

SEQUENCE LISTING



#3

<110> Shimkets, Richard  
Fernandes, Elma  
Vernet, Corine  
Yang, Meijia  
Boldog, Ferenc  
Herrmann, John

<120> Novel Nucleic Acid Sequences Encoding Human Semaphorin-Like Polypeptides

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<141> 2001-11-02

<150> 09/604,286

<151> 2000-06-22

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<170> PatentIn Ver. 2.0

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Met Thr Ile His Gln Phe Leu Leu Leu Phe  
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Leu Phe Trp Val Cys Leu Pro His Phe Cys Ser Pro Glu Ile Met Phe  
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agg agt gat ggc aaa att ctc cat cgt caa aaa cgt ggt tgg atg tgg 437  
Arg Ser Asp Gly Lys Ile Leu His Arg Gln Lys Arg Gly Trp Met Trp  
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aat caa ttt ttc tta ctt gaa gaa tat aca gga tct gat tat cag tac 485  
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Val Gly Lys Leu His Ser Asp Gln Asp Lys Gly Asp Gly Ser Leu Lys  
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tat atc tta tct gga gat gga gct ggt act ctt ttt att att gat gaa 581  
Tyr Ile Leu Ser Gly Asp Gly Ala Gly Thr Leu Phe Ile Ile Asp Glu  
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Lys Thr Gly Asp Ile His Ala Thr Arg Arg Ile Asp Arg Glu Glu Lys  
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 Thr Glu Lys Asp Thr Gln Glu Gly Ile Ile Thr Val Lys Lys Pro Leu  
 325 330 335  
 Asp Tyr Glu Ser Arg Arg Leu Tyr Thr Leu Lys Val Glu Ala Glu Asn  
 340 345 350

Thr His Val Asp Pro Arg Phe Tyr Tyr Leu Gly Pro Phe Lys Asp Thr  
 355 360 365  
 Thr Ile Val Lys Ile Ser Ile Glu Asp Val Asp Glu Pro Pro Val Phe  
 370 375 380  
 Ser Arg Ser Ser Tyr Leu Phe Glu Val His Glu Asp Ile Glu Val Gly  
 385 390 395 400  
 Thr Ile Ile Gly Thr Val Met Ala Arg Asp Pro Asp Ser Ile Ser Ser  
 405 410 415  
 Pro Ile Arg Phe Ser Leu Asp Arg His Thr Asp Leu Asp Arg Ile Phe  
 420 425 430  
 Asn Ile His Ser Gly Asn Gly Ser Leu Tyr Thr Ser Lys Pro Leu Asp  
 435 440 445  
 Arg Glu Leu Ser Gln Trp His Asn Ser Leu Val Ile Ala Ala Glu Ile  
 450 455 460  
 Asn Asn Pro Lys Glu Thr Thr Arg Val Ala Val Phe Val Arg Ile Leu  
 465 470 475 480  
 Asp Val Asn Asp Asn Ala Pro Gln Phe Ala Val Phe Tyr Asp Thr Phe  
 485 490 495  
 Val Cys Glu Asn Ala Arg Pro Gly Gln Leu Ile Gln Thr Ile Ser Ala  
 500 505 510  
 Val Asp Lys Asp Asp Pro Leu Gly Gly Gln Lys Phe Phe Phe Ser Leu  
 515 520 525  
 Ala Ala Val Asn Pro Asn Phe Thr Val Gln Asp Asn Glu Asp Asn Thr  
 530 535 540  
 Ala Arg Ile Leu Thr Arg Lys Asn Gly Phe Asn Arg His Glu Ile Ser  
 545 550 555 560  
 Thr Tyr Leu Leu Pro Val Val Ile Ser Asp Asn Asp Tyr Pro Ile Gln  
 565 570 575  
 Ser Ser Thr Gly Thr Leu Thr Ile Arg Val Cys Ala Cys Asp Ser Gln  
 580 585 590  
 Gly Asn Met Gln Ser Cys Ser Ala Glu Ala Leu Leu Leu Pro Ala Gly  
 595 600 605  
 Leu Ser Thr Gly Ala Leu Ile Ala Ile Leu Leu Cys Ile Ile Ile Leu  
 610 615 620  
 Leu Val Ile Val Val Leu Phe Ala Ala Leu Lys Gly Gln Arg Lys Lys  
 625 630 635 640  
 Glu Pro Leu Ile Leu Ser Lys Glu Asp Ile Arg Asp Asn Ile Val Ser  
 645 650 655

Tyr Asn Asp Glu Gly Gly Gly Glu Glu Asp Thr Gln Ala Phe Asp Ile  
 660 665 670  
 Gly Thr Leu Arg Asn Pro Ala Ala Ile Glu Glu Lys Lys Leu Arg Arg  
 675 680 685  
 Asp Ile Ile Pro Glu Thr Leu Phe Ile Pro Arg Arg Thr Pro Thr Ala  
 690 695 700  
 Pro Asp Asn Thr Asp Val Arg Asp Phe Ile Asn Glu Arg Leu Lys Glu  
 705 710 715 720  
 His Asp Leu Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Ala Thr Tyr  
 725 730 735  
 Ala Tyr Glu Gly Asn Asp Ser Ile Ala Glu Ser Leu Ser Ser Leu Glu  
 740 745 750  
 Ser Gly Thr Thr Glu Gly Asp Gln Asn Tyr Asp Tyr Leu Arg Glu Trp  
 755 760 765  
 Gly Pro Arg Phe Asn Lys Leu Ala Glu Met Tyr Gly Gly Gly Glu Ser  
 770 775 780  
 Asp Lys Asp Ser  
 785

<210> 7  
 <211> 1820  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (285)..(1703)

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 atgcctctta ggaaatgact tccaacatgt agtacactat tcatcttcga gttcttgaat 180  
 cctccccagt tggcacagcc attggaagtg tcaaagcaac tgatgctgac actgggaaaa 240  
 atgctgaagt agaataccga attattgatg gtgacgggtac tgat atg ttt gac atc 296  
 Met Phe Asp Ile  
 1

gtg act gag aag gac aca cag gaa ggc atc atc act gtg aaa aag cca 344  
 Val Thr Glu Lys Asp Thr Gln Glu Gly Ile Ile Thr Val Lys Lys Pro  
 5 10 15 20  
 ctc gac tat gag agc cga aga ctt tat act ctg aaa gtc gaa gca gaa 392  
 Leu Asp Tyr Glu Ser Arg Arg Leu Tyr Thr Leu Lys Val Glu Ala Glu  
 25 30 35

aac acc cat gta gat ccc cgt ttt tat tac cta gga cca ttt aaa gat 440  
 Asn Thr His Val Asp Pro Arg Phe Tyr Tyr Leu Gly Pro Phe Lys Asp  
 40 45 50

act acc ata gtg aaa atc tct ata gaa gat gtg gat gaa cct cct gtt 488  
 Thr Thr Ile Val Lys Ile Ser Ile Glu Asp Val Asp Glu Pro Pro Val  
 55 60 65

ttt agt agg tcc tcc tat ctg ttt gaa gtt cat gaa gat att gaa gtg 536  
 Phe Ser Arg Ser Ser Tyr Leu Phe Glu Val His Glu Asp Ile Glu Val  
 70 75 80

ggc aca atc att ggt act gta atg gca agg gac cca gat tct att tcc 584  
 Gly Thr Ile Ile Gly Thr Val Met Ala Arg Asp Pro Asp Ser Ile Ser  
 85 90 95 100

agc ccc att aga ttt tcc ttg gat cgc cat act gac ctt gac aga atc 632  
 Ser Pro Ile Arg Phe Ser Leu Asp Arg His Thr Asp Leu Asp Arg Ile  
 105 110 115

ttt aac att cat tca gga aat gga tct ctt tat aca tca aaa cct ctt 680  
 Phe Asn Ile His Ser Gly Asn Gly Ser Leu Tyr Thr Ser Lys Pro Leu  
 120 125 130

gac cgt gaa cta tct cag tgg cat aat tcg tta gtt att gct gct gaa 728  
 Asp Arg Glu Leu Ser Gln Trp His Asn Ser Leu Val Ile Ala Ala Glu  
 135 140 145

atc aac aat ccc aaa gag aca aca cgc gtg gct gtt ttt gtg aga att 776  
 Ile Asn Asn Pro Lys Glu Thr Thr Arg Val Ala Val Phe Val Arg Ile  
 150 155 160

ttg gat gtt aat gac aat gcc cca cag ttt gct gtg ttc tat gac act 824  
 Leu Asp Val Asn Asp Asn Ala Pro Gln Phe Ala Val Phe Tyr Asp Thr  
 165 170 175 180

ttt gta tgt gaa aat gcc aga cca ggg cag cta ata cag act ata agt 872  
 Phe Val Cys Glu Asn Ala Arg Pro Gly Gln Leu Ile Gln Thr Ile Ser  
 185 190 195

gca gta gac aaa gat gac cct tta ggt gga cag aaa ttt ttt ttc agt 920  
 Ala Val Asp Lys Asp Asp Pro Leu Gly Gly Gln Lys Phe Phe Phe Ser  
 200 205 210

tta gct gct gtc aat cca aac ttc aca gta cag gat aat gaa gat aat 968  
 Leu Ala Ala Val Asn Pro Asn Phe Thr Val Gln Asp Asn Glu Asp Asn  
 215 220 225

act gcc aga atc tta acc aga aaa aat gga ttc aat aga cat gaa atc 1016  
 Thr Ala Arg Ile Leu Thr Arg Lys Asn Gly Phe Asn Arg His Glu Ile  
 230 235 240

agt acc tat ctc ttg cct gtg gtg ata tca gac aat gat tac ccg att 1064  
 Ser Thr Tyr Leu Leu Pro Val Val Ile Ser Asp Asn Asp Tyr Pro Ile  
 245 250 255 260

cag agc agc aca ggc aca ctg acc att cga gtg tgt gct tgt gac agc 1112  
Gln Ser Ser Thr Gly Thr Leu Thr Ile Arg Val Cys Ala Cys Asp Ser  
265 270 275

caa ggc aac atg caa tcc tgc agt gct gaa gcc ctg ctc ctc cct gcc 1160  
Gln Gly Asn Met Gln Ser Cys Ser Ala Glu Ala Leu Leu Leu Pro Ala  
280 285 290

ggc ctc agc act ggg gcc ttg atc gcc atc ctc ctc tgc atc atc att 1208  
Gly Leu Ser Thr Gly Ala Leu Ile Ala Ile Leu Leu Cys Ile Ile Ile  
295 300 305

cta ctg gtt ata gta gta ctg ttt gca gct ctg aaa gga cag cga aaa 1256  
Leu Leu Val Ile Val Val Leu Phe Ala Ala Leu Lys Gly Gln Arg Lys  
310 315 320

aaa gag cct ctg atc ttg tca aaa gaa gat atc aga gac aac att gtg 1304  
Lys Glu Pro Leu Ile Leu Ser Lys Glu Asp Ile Arg Asp Asn Ile Val  
325 330 335 340

agc tat aac gat gag ggt ggt gga gag gag gac acc cag gcc ttt gat 1352  
Ser Tyr Asn Asp Glu Gly Gly Gly Glu Glu Asp Thr Gln Ala Phe Asp  
345 350 355

atc ggc acc ctg agg aat cct gca gcc att gag gaa aaa aag ctc cgg 1400  
Ile Gly Thr Leu Arg Asn Pro Ala Ala Ile Glu Glu Lys Lys Leu Arg  
360 365 370

cga gat att att cca gaa acg tta ttt att cct cgg agg act cct aca 1448  
Arg Asp Ile Ile Pro Glu Thr Leu Phe Ile Pro Arg Arg Thr Pro Thr  
375 380 385

gct cca gat aac acg gac gtc cgg gat ttc att aat gaa agg cta aaa 1496  
Ala Pro Asp Asn Thr Asp Val Arg Asp Phe Ile Asn Glu Arg Leu Lys  
390 395 400

gag cat gat ctt gac ccc acc gca ccc ccc tac gac tca ctt gca acc 1544  
Glu His Asp Leu Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Ala Thr  
405 410 415 420

tat gcc tat gaa gga aat gat tcc att gct gaa tct ctg agt tca tta 1592  
Tyr Ala Tyr Glu Gly Asn Asp Ser Ile Ala Glu Ser Leu Ser Ser Leu  
425 430 435

gaa tca ggt act act gaa gga gac caa aac tac gat tac ctc cga gaa 1640  
Glu Ser Gly Thr Thr Glu Gly Asp Gln Asn Tyr Asp Tyr Leu Arg Glu  
440 445 450

tgg ggc cct cgg ttt aat aag cta gca gaa atg tat ggt ggt ggg gaa 1688  
Trp Gly Pro Arg Phe Asn Lys Leu Ala Glu Met Tyr Gly Gly Gly Glu  
455 460 465

agc gac aaa gac tct taacgtagga tatatgttct gttcaaaca gagaaagtaa 1743  
Ser Asp Lys Asp Ser  
470

ctctacccat gctgtctcca cttcacaata tttgatattc aggagcattt cctgcagtca 1803

gcacaattttt tttctca

1820

<210> 8  
<211> 473  
<212> PRT  
<213> Homo sapiens

<400> 8

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Val Lys Lys Pro Leu Asp Tyr Glu Ser Arg Arg Leu Tyr Thr Leu Lys  
20 25 30  
Val Glu Ala Glu Asn Thr His Val Asp Pro Arg Phe Tyr Tyr Leu Gly  
35 40 45  
Pro Phe Lys Asp Thr Thr Ile Val Lys Ile Ser Ile Glu Asp Val Asp  
50 55 60  
Glu Pro Pro Val Phe Ser Arg Ser Ser Tyr Leu Phe Glu Val His Glu  
65 70 75 80  
Asp Ile Glu Val Gly Thr Ile Ile Gly Thr Val Met Ala Arg Asp Pro  
85 90 95  
Asp Ser Ile Ser Ser Pro Ile Arg Phe Ser Leu Asp Arg His Thr Asp  
100 105 110  
Leu Asp Arg Ile Phe Asn Ile His Ser Gly Asn Gly Ser Leu Tyr Thr  
115 120 125  
Ser Lys Pro Leu Asp Arg Glu Leu Ser Gln Trp His Asn Ser Leu Val  
130 135 140  
Ile Ala Ala Glu Ile Asn Asn Pro Lys Glu Thr Thr Arg Val Ala Val  
145 150 155 160  
Phe Val Arg Ile Leu Asp Val Asn Asp Asn Ala Pro Gln Phe Ala Val  
165 170 175  
Phe Tyr Asp Thr Phe Val Cys Glu Asn Ala Arg Pro Gly Gln Leu Ile  
180 185 190  
Gln Thr Ile Ser Ala Val Asp Lys Asp Asp Pro Leu Gly Gly Gln Lys  
195 200 205  
Phe Phe Phe Ser Leu Ala Ala Val Asn Pro Asn Phe Thr Val Gln Asp  
210 215 220  
Asn Glu Asp Asn Thr Ala Arg Ile Leu Thr Arg Lys Asn Gly Phe Asn  
225 230 235 240  
Arg His Glu Ile Ser Thr Tyr Leu Leu Pro Val Val Ile Ser Asp Asn  
245 250 255

Asp Tyr Pro Ile Gln Ser Ser Thr Gly Thr Leu Thr Ile Arg Val Cys  
 260 265 270  
 Ala Cys Asp Ser Gln Gly Asn Met Gln Ser Cys Ser Ala Glu Ala Leu  
 275 280 285  
 Leu Leu Pro Ala Gly Leu Ser Thr Gly Ala Leu Ile Ala Ile Leu Leu  
 290 295 300  
 Cys Ile Ile Ile Leu Leu Val Ile Val Val Leu Phe Ala Ala Leu Lys  
 305 310 315 320  
 Gly Gln Arg Lys Lys Glu Pro Leu Ile Leu Ser Lys Glu Asp Ile Arg  
 325 330 335  
 Asp Asn Ile Val Ser Tyr Asn Asp Glu Gly Gly Gly Glu Glu Asp Thr  
 340 345 350  
 Gln Ala Phe Asp Ile Gly Thr Leu Arg Asn Pro Ala Ala Ile Glu Glu  
 355 360 365  
 Lys Lys Leu Arg Arg Asp Ile Ile Pro Glu Thr Leu Phe Ile Pro Arg  
 370 375 380  
 Arg Thr Pro Thr Ala Pro Asp Asn Thr Asp Val Arg Asp Phe Ile Asn  
 385 390 395 400  
 Glu Arg Leu Lys Glu His Asp Leu Asp Pro Thr Ala Pro Pro Tyr Asp  
 405 410 415  
 Ser Leu Ala Thr Tyr Ala Tyr Glu Gly Asn Asp Ser Ile Ala Glu Ser  
 420 425 430  
 Leu Ser Ser Leu Glu Ser Gly Thr Thr Glu Gly Asp Gln Asn Tyr Asp  
 435 440 445  
 Tyr Leu Arg Glu Trp Gly Pro Arg Phe Asn Lys Leu Ala Glu Met Tyr  
 450 455 460  
 Gly Gly Gly Glu Ser Asp Lys Asp Ser  
 465 470

<210> 9  
 <211> 1508  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (226)..(1458)

<220>  
 <221> variation  
 <222> (1)..(1508)  
 <223> N may be any nucleotide



<400> 9

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caattttaat agtccgtaat tgatggcagc ctgctgtggt acatgtgtga aagattatca 120  
ctttgaatat acggaatgtg atagcagtggt ctccaggtgg agagttgcca ttccaaattc 180  
tgcagtgagac tgctctggcc tgcctgaccc agtgagagggc aaaga atg cac tct tct 237  
Met His Ser Ser

1

tgg atc cct cgt gga aac tac ata gaa tct aat cgt gat gac tgc acg 285  
Trp Ile Pro Arg Gly Asn Tyr Ile Glu Ser Asn Arg Asp Asp Cys Thr  
5 10 15 20

gtg tct ttg atc tat gct gtg cac ctt aag aag tca ggc tat gtc ttc 333  
Val Ser Leu Ile Tyr Ala Val His Leu Lys Lys Ser Gly Tyr Val Phe  
25 30 35

ttt gag tac cag tat gtc gac aac aac atc ttc ttt gag ttc ttt att 381  
Phe Glu Tyr Gln Tyr Val Asp Asn Asn Ile Phe Phe Glu Phe Phe Ile  
40 45 50

caa aat gat cag tgc cag gag atg gac acc acc act gac aag tgg gta 429  
Gln Asn Asp Gln Cys Gln Glu Met Asp Thr Thr Thr Asp Lys Trp Val  
55 60 65

aaa ctt aca gac aat gga gaa tgg ggc tct cat tct gta atg ctg aaa 477  
Lys Leu Thr Asp Asn Gly Glu Trp Gly Ser His Ser Val Met Leu Lys  
70 75 80

tca ggc aca aac ata ctc tac tgg aga act aca ggc atc ctt atg ggt 525  
Ser Gly Thr Asn Ile Leu Tyr Trp Arg Thr Thr Gly Ile Leu Met Gly  
85 90 95 100

tct aag gcg gtc aag cct gtg ctg gta aaa aat atc aca att gaa ggg 573  
Ser Lys Ala Val Lys Pro Val Leu Val Lys Asn Ile Thr Ile Glu Gly  
105 110 115

gtg gcg tac aca tca gaa tgt ttt cct tgc aag cca ggc aca ttc agc 621  
Val Ala Tyr Thr Ser Glu Cys Phe Pro Cys Lys Pro Gly Thr Phe Ser  
120 125 130

aac aaa cca ggt tca ttc aac tgc cag gtg tgt ccc aga aac acc tat 669  
Asn Lys Pro Gly Ser Phe Asn Cys Gln Val Cys Pro Arg Asn Thr Tyr  
135 140 145

tct gag aaa gga gcc aaa gaa tgt ata agg tgt aaa gac gac tct caa 717  
Ser Glu Lys Gly Ala Lys Glu Cys Ile Arg Cys Lys Asp Asp Ser Gln  
150 155 160

ttt tca gag gaa gga tcc agt gag tgt aca gag cgc cct ccc tgt acc 765  
Phe Ser Glu Glu Gly Ser Ser Glu Cys Thr Glu Arg Pro Pro Cys Thr  
165 170 175 180

aca aaa gac tat ttc cag atc cat act cca tgt gat gaa gaa gga aag 813

Thr	Lys	Asp	Tyr	Phe	Gln	Ile	His	Thr	Pro	Cys	Asp	Glu	Glu	Gly	Lys		
				185					190					195			
aca	cag	ata	atg	tac	aag	tgg	ata	gag	ccc	aaa	atc	tgc	cgg	gag	gat	861	
Thr	Gln	Ile	Met	Tyr	Lys	Trp	Ile	Glu	Pro	Lys	Ile	Cys	Arg	Glu	Asp		
			200					205					210				
ctc	aca	gat	gct	att	aga	ttg	ccc	cct	tct	gga	gag	aag	aag	gat	tgt	909	
Leu	Thr	Asp	Ala	Ile	Arg	Leu	Pro	Pro	Ser	Gly	Glu	Lys	Lys	Asp	Cys		
			215				220						225				
ccg	cct	tgc	aac	cct	gga	ttt	tat	aac	aat	gga	tca	tct	tct	tgc	cat	957	
Pro	Pro	Cys	Asn	Pro	Gly	Phe	Tyr	Asn	Asn	Gly	Ser	Ser	Ser	Cys	His		
			230				235					240					
ccc	tgt	cct	cct	gga	aca	ttt	tca	gat	gga	acc	aaa	gaa	tgt	aga	cca	1005	
Pro	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Asp	Gly	Thr	Lys	Glu	Cys	Arg	Pro		
					250					255					260		
tgt	cca	gca	gga	acg	gag	cct	gca	ctt	ggc	ttt	gaa	tat	aaa	tgg	tgg	1053	
Cys	Pro	Ala	Gly	Thr	Glu	Pro	Ala	Leu	Gly	Phe	Glu	Tyr	Lys	Trp	Trp		
				265					270					275			
aat	gtc	ctt	cct	ggc	aac	atg	aaa	act	tcc	tgc	ttc	aat	gtt	ggg	aat	1101	
Asn	Val	Leu	Pro	Gly	Asn	Met	Lys	Thr	Ser	Cys	Phe	Asn	Val	Gly	Asn		
				280				285						290			
tca	aag	tgc	gat	gga	atg	aat	ggg	tgg	gag	gtg	gct	gga	gat	cat	atc	1149	
Ser	Lys	Cys	Asp	Gly	Met	Asn	Gly	Trp	Glu	Val	Ala	Gly	Asp	His	Ile		
			295				300					305					
cag	agt	ggg	gct	gga	ggg	tct	gac	aat	gat	tac	ctg	atc	tta	aac	ttg	1197	
Gln	Ser	Gly	Ala	Gly	Gly	Ser	Asp	Asn	Asp	Tyr	Leu	Ile	Leu	Asn	Leu		
			310				315					320					
cat	atc	cca	gga	ttt	aaa	cca	cca	aca	tct	atg	act	gga	gcc	acg	ggg	1245	
His	Ile	Pro	Gly	Phe	Lys	Pro	Pro	Thr	Ser	Met	Thr	Gly	Ala	Thr	Gly		
					330					335					340		
tct	gaa	cta	gga	aga	ata	aca	ttt	gtc	ttt	gag	acc	ctc	tgt	tca	gct	1293	
Ser	Glu	Leu	Gly	Arg	Ile	Thr	Phe	Val	Phe	Glu	Thr	Leu	Cys	Ser	Ala		
				345				350						355			
gac	tgt	gtt	ttg	tac	ttc	atg	gtg	gat	att	aat	aga	aaa	agt	aca	aat	1341	
Asp	Cys	Val	Leu	Tyr	Phe	Met	Val	Asp	Ile	Asn	Arg	Lys	Ser	Thr	Asn		
				360				365					370				
gtg	gta	gaa	tcg	tgg	ggg	gga	acc	aaa	gaa	aaa	caa	gct	tac	acc	cat	1389	
Val	Val	Glu	Ser	Trp	Gly	Gly	Thr	Lys	Glu	Lys	Gln	Ala	Tyr	Thr	His		
			375				380					385					
atc	atc	ttc	aag	aat	gca	act	ttt	aca	ttt	aca	tgg	ggc	att	ccc	aga	1437	
Ile	Ile	Phe	Lys	Asn	Ala	Thr	Phe	Thr	Phe	Thr	Trp	Gly	Ile	Pro	Arg		
			390				395				400						
gaa	cta	att	cag	ggg	cca	aga	taatagacgg	ttccnccatt	gacatgtttg							1488	
Glu	Leu	Ile	Gln	Gly	Pro	Arg											

405

410

aaggatttat tcctattcac

1508

&lt;210&gt; 10

&lt;211&gt; 411

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 10

Met His Ser Ser Trp Ile Pro Arg Gly Asn Tyr Ile Glu Ser Asn Arg  
 1 5 10 15

Asp Asp Cys Thr Val Ser Leu Ile Tyr Ala Val His Leu Lys Lys Ser  
 20 25 30

Gly Tyr Val Phe Phe Glu Tyr Gln Tyr Val Asp Asn Asn Ile Phe Phe  
 35 40 45

Glu Phe Phe Ile Gln Asn Asp Gln Cys Gln Glu Met Asp Thr Thr Thr  
 50 55 60

Asp Lys Trp Val Lys Leu Thr Asp Asn Gly Glu Trp Gly Ser His Ser  
 65 70 75 80

Val Met Leu Lys Ser Gly Thr Asn Ile Leu Tyr Trp Arg Thr Thr Gly  
 85 90 95

Ile Leu Met Gly Ser Lys Ala Val Lys Pro Val Leu Val Lys Asn Ile  
 100 105 110

Thr Ile Glu Gly Val Ala Tyr Thr Ser Glu Cys Phe Pro Cys Lys Pro  
 115 120 125

Gly Thr Phe Ser Asn Lys Pro Gly Ser Phe Asn Cys Gln Val Cys Pro  
 130 135 140

Arg Asn Thr Tyr Ser Glu Lys Gly Ala Lys Glu Cys Ile Arg Cys Lys  
 145 150 155 160

Asp Asp Ser Gln Phe Ser Glu Glu Gly Ser Ser Glu Cys Thr Glu Arg  
 165 170 175

Pro Pro Cys Thr Thr Lys Asp Tyr Phe Gln Ile His Thr Pro Cys Asp  
 180 185 190

Glu Glu Gly Lys Thr Gln Ile Met Tyr Lys Trp Ile Glu Pro Lys Ile  
 195 200 205

Cys Arg Glu Asp Leu Thr Asp Ala Ile Arg Leu Pro Pro Ser Gly Glu  
 210 215 220

Lys Lys Asp Cys Pro Pro Cys Asn Pro Gly Phe Tyr Asn Asn Gly Ser  
 225 230 235 240

Ser Ser Cys His Pro Cys Pro Pro Gly Thr Phe Ser Asp Gly Thr Lys

245					250					255					
Glu	Cys	Arg	Pro	Cys	Pro	Ala	Gly	Thr	Glu	Pro	Ala	Leu	Gly	Phe	Glu
			260					265					270		
Tyr	Lys	Trp	Trp	Asn	Val	Leu	Pro	Gly	Asn	Met	Lys	Thr	Ser	Cys	Phe
		275					280					285			
Asn	Val	Gly	Asn	Ser	Lys	Cys	Asp	Gly	Met	Asn	Gly	Trp	Glu	Val	Ala
		290					295					300			
Gly	Asp	His	Ile	Gln	Ser	Gly	Ala	Gly	Gly	Ser	Asp	Asn	Asp	Tyr	Leu
305						310					315				320
Ile	Leu	Asn	Leu	His	Ile	Pro	Gly	Phe	Lys	Pro	Pro	Thr	Ser	Met	Thr
				325					330					335	
Gly	Ala	Thr	Gly	Ser	Glu	Leu	Gly	Arg	Ile	Thr	Phe	Val	Phe	Glu	Thr
			340					345					350		
Leu	Cys	Ser	Ala	Asp	Cys	Val	Leu	Tyr	Phe	Met	Val	Asp	Ile	Asn	Arg
		355					360					365			
Lys	Ser	Thr	Asn	Val	Val	Glu	Ser	Trp	Gly	Gly	Thr	Lys	Glu	Lys	Gln
		370					375					380			
Ala	Tyr	Thr	His	Ile	Ile	Phe	Lys	Asn	Ala	Thr	Phe	Thr	Phe	Thr	Trp
385						390					395				400
Gly	Ile	Pro	Arg	Glu	Leu	Ile	Gln	Gly	Pro	Arg					
			405						410						

<210> 11  
 <211> 2155  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (166)..(1935)

<400> 11  
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 attgtctgcg ctggggaagg ggacaggccg ggaccgggac ctccgctcgc agccggccgc 120  
 accagcagga cagctggcct gaagctcaga gccggggcgt gcgcc atg gcc cca cac 177  
 Met Ala Pro His  
 1

tgg gct gtc tgg ctg ctg gca gca agg ctg tgg ggc ctg ggc att ggg 225  
 Trp Ala Val Trp Leu Leu Ala Ala Arg Leu Trp Gly Leu Gly Ile Gly  
 5 10 15 20  
 gct gag gtg tgg tgg aac ctt gtg ccg cgt aag aca gtg tct tct ggg 273  
 Ala Glu Val Trp Trp Asn Leu Val Pro Arg Lys Thr Val Ser Ser Gly

25										30					35					
gag	ctg	gcc	acg	gta	gta	cgg	cgg	ttc	tcc	cag	acc	ggc	atc	cag	gac	321				
Glu	Leu	Ala	Thr	Val	Val	Arg	Arg	Phe	Ser	Gln	Thr	Gly	Ile	Gln	Asp					
			40			45						50								
ttc	ctg	aca	ctg	acg	ctg	acg	gag	ccc	act	ggg	ctt	ctg	tac	gtg	ggc	369				
Phe	Leu	Thr	Leu	Thr	Leu	Thr	Glu	Pro	Thr	Gly	Leu	Leu	Tyr	Val	Gly					
			55			60						65								
gcc	cga	gag	gcc	ctg	ttt	gcc	ttc	agc	atg	gag	gcc	ctg	gag	ctg	caa	417				
Ala	Arg	Glu	Ala	Leu	Phe	Ala	Phe	Ser	Met	Glu	Ala	Leu	Glu	Leu	Gln					
			70			75						80								
gga	gcg	atc	tcc	tgg	gag	gcc	ccc	gtg	gag	aag	aag	act	gag	tgt	atc	465				
Gly	Ala	Ile	Ser	Trp	Glu	Ala	Pro	Val	Glu	Lys	Lys	Thr	Glu	Cys	Ile					
85					90					95					100					
cag	aaa	ggg	aag	aac	aac	cag	acc	gag	tgc	ttc	aac	ttc	atc	cgc	ttc	513				
Gln	Lys	Gly	Lys	Asn	Asn	Gln	Thr	Glu	Cys	Phe	Asn	Phe	Ile	Arg	Phe					
			105						110						115					
ctg	cag	ccc	tac	aat	gcc	tcc	cac	ctg	tac	gtc	tgt	ggc	acc	tac	gcc	561				
Leu	Gln	Pro	Tyr	Asn	Ala	Ser	His	Leu	Tyr	Val	Cys	Gly	Thr	Tyr	Ala					
			120						125						130					
ttc	cag	ccc	aag	tgc	acc	tac	gtc	aac	atg	ctc	acc	ttc	act	ttg	gag	609				
Phe	Gln	Pro	Lys	Cys	Thr	Tyr	Val	Asn	Met	Leu	Thr	Phe	Thr	Leu	Glu					
			135						140						145					
cat	gga	gag	ttt	gaa	gat	ggg	aag	ggc	aag	tgt	ccc	tat	gac	cca	gct	657				
His	Gly	Glu	Phe	Glu	Asp	Gly	Lys	Gly	Lys	Cys	Pro	Tyr	Asp	Pro	Ala					
150					155						160									
aag	ggc	cat	gct	ggc	ctt	ctt	gtg	gat	ggg	gag	ctg	tac	tcg	gcc	aca	705				
Lys	Gly	His	Ala	Gly	Leu	Leu	Val	Asp	Gly	Glu	Leu	Tyr	Ser	Ala	Thr					
165					170						175			180						
ctc	aac	aac	ttc	ctg	ggc	acg	gaa	ccc	att	atc	ctg	cgt	aac	atg	ggg	753				
Leu	Asn	Asn	Phe	Leu	Gly	Thr	Glu	Pro	Ile	Ile	Leu	Arg	Asn	Met	Gly					
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ccc	cac	cac	tcc	atg	aag	aca	gag	tac	ctg	gcc	ttt	tgg	ctc	aac	gaa	801				
Pro	His	His	Ser	Met	Lys	Thr	Glu	Tyr	Leu	Ala	Phe	Trp	Leu	Asn	Glu					
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cct	cac	ttt	gta	ggc	tct	gcc	tat	gta	cct	gag	agt	gtg	ggc	agc	ttc	849				
Pro	His	Phe	Val	Gly	Ser	Ala	Tyr	Val	Pro	Glu	Ser	Val	Gly	Ser	Phe					
			215						220						225					
acg	ggg	gac	gac	gac	aag	gtc	tac	ttc	ttc	ttc	agg	gag	cgg	gca	gtg	897				
Thr	Gly	Asp	Asp	Asp	Lys	Val	Tyr	Phe	Phe	Phe	Arg	Glu	Arg	Ala	Val					
230					235						240									
gag	tcc	gac	tgc	tat	gcc	gag	cag	gtg	gtg	gct	cgt	gtg	gcc	cgt	gtc	945				
Glu	Ser	Asp	Cys	Tyr	Ala	Glu	Gln	Val	Val	Ala	Arg	Val	Ala	Arg	Val					
245					250						255			260						

tgc aag ggc gat atg ggg ggc gca cgg acc ctg cag agg aag tgg acc	993
Cys Lys Gly Asp Met Gly Gly Ala Arg Thr Leu Gln Arg Lys Trp Thr	
265 270 275	
acg ttc ctg aag gcg cgg ctg gca tgc tct gcc ccg aac tgg cag ctc	1041
Thr Phe Leu Lys Ala Arg Leu Ala Cys Ser Ala Pro Asn Trp Gln Leu	
280 285 290	
tac ttc aac cag ctg cag gcg atg cac acc ctg cag gac acc tcc tgg	1089
Tyr Phe Asn Gln Leu Gln Ala Met His Thr Leu Gln Asp Thr Ser Trp	
295 300 305	
cac aac acc acc ttc ttt ggg gtt ttt caa gca cag tgg ggt gac atg	1137
His Asn Thr Thr Phe Phe Gly Val Phe Gln Ala Gln Trp Gly Asp Met	
310 315 320	
tac ctg tgc gcc atc tgt gag tac cag ttg gaa gag atc cag cgg gtg	1185
Tyr Leu Ser Ala Ile Cys Glu Tyr Gln Leu Glu Glu Ile Gln Arg Val	
325 330 335 340	
ttt gag ggc ccc tat aag gag tac cat gag gaa gcc cag aag tgg gac	1233
Phe Glu Gly Pro Tyr Lys Glu Tyr His Glu Glu Ala Gln Lys Trp Asp	
345 350 355	
cgc tac act gac cct gta ccc agc cct cgg cct ggc tgc tgc att aac	1281
Arg Tyr Thr Asp Pro Val Pro Ser Pro Arg Pro Gly Ser Cys Ile Asn	
360 365 370	
aac tgg cat cgg cgc cac ggc tac acc agc tcc ctg gag cta ccc gac	1329
Asn Trp His Arg Arg His Gly Tyr Thr Ser Ser Leu Glu Leu Pro Asp	
375 380 385	
aac atc ctc aac ttc gtc aag aag cac ccg ctg atg gag gag cag gtg	1377
Asn Ile Leu Asn Phe Val Lys Lys His Pro Leu Met Glu Glu Gln Val	
390 395 400	
ggg cct cgg tgg agc cgc ccc ctg ctc gtg aag aag ggc acc aac ttc	1425
Gly Pro Arg Trp Ser Arg Pro Leu Leu Val Lys Lys Gly Thr Asn Phe	
405 410 415 420	
acc cac ctg gtg gcc gac cgg gtt aca gga ctt gat gga gcc acc tat	1473
Thr His Leu Val Ala Asp Arg Val Thr Gly Leu Asp Gly Ala Thr Tyr	
425 430 435	
aca gtg ctg ttc att ggc aca gga gac ggc tgg ctg ctc aag gct gtg	1521
Thr Val Leu Phe Ile Gly Thr Gly Asp Gly Trp Leu Leu Lys Ala Val	
440 445 450	
agc ctg ggg ccc tgg gtt cac ctg att gag gag ctg cag ctg ttt gac	1569
Ser Leu Gly Pro Trp Val His Leu Ile Glu Glu Leu Gln Leu Phe Asp	
455 460 465	
cag gag ccc atg aga agc ctg gtg cta tct cag agc aag aag ctg ctc	1617
Gln Glu Pro Met Arg Ser Leu Val Leu Ser Gln Ser Lys Lys Leu Leu	
470 475 480	

ttt gcc ggc tcc cgc tct cag ctg gtg cag ctg ccc gtg gcc gac tgc 1665  
Phe Ala Gly Ser Arg Ser Gln Leu Val Gln Leu Pro Val Ala Asp Cys  
485 490 495 500

ata aag tat cgc tcc tgt gca gac tgt gtc ctc gcc cgg gac ccc tat 1713  
Ile Lys Tyr Arg Ser Cys Ala Asp Cys Val Leu Ala Arg Asp Pro Tyr  
505 510 515

tgc gcc tgg agc gtc aac acc agc cgc tgt gtg gcc gtg ggt ggc cac 1761  
Cys Ala Trp Ser Val Asn Thr Ser Arg Cys Val Ala Val Gly Gly His  
520 525 530

ttt gga tct tta ctg atc cag cat gtg atg acc tcg gac act tca ggc 1809  
Phe Gly Ser Leu Leu Ile Gln His Val Met Thr Ser Asp Thr Ser Gly  
535 540 545

att tgc aac ctc cgt ggc agt aag aaa gtc agg ccc act ccc aaa aac 1857  
Ile Cys Asn Leu Arg Gly Ser Lys Lys Val Arg Pro Thr Pro Lys Asn  
550 555 560

atc acg gtg gtg gcg ggc aca gac ctg gtg ctg ccc tgc cac ctc tcc 1905  
Ile Thr Val Val Ala Gly Thr Asp Leu Val Leu Pro Cys His Leu Ser  
565 570 575 580

tcc act tgg ccc cgg ggt tca gtg gta ttt taaacttgcc ttcttctgt 1955  
Ser Thr Trp Pro Arg Gly Ser Val Val Phe  
585 590

acagggctgg gaaaggctgt gttaggggaa aaaaaggaaa ggggtgggcct gctgtggaca 2015

atggcatact ctcttccagc cctaggagga gggctcctaa cagtgttaact tattgtgtcc 2075

ccgcgtatatt atttgttgta aatatttgag tattttttata ttgacaaata aaatggagaa 2135

aatgaaaaaa aaaaaaaaaa 2155

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<212> PRT  
<213> Homo sapiens

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Val Ser Ser Gly Glu Leu Ala Thr Val Val Arg Arg Phe Ser Gln Thr  
35 40 45  
Gly Ile Gln Asp Phe Leu Thr Leu Thr Leu Thr Glu Pro Thr Gly Leu  
50 55 60  
Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Phe Ser Met Glu Ala  
65 70 75 80

Leu Glu Leu Gln Gly Ala Ile Ser Trp Glu Ala Pro Val Glu Lys Lys  
                                     85                                    90                                    95  
 Thr Glu Cys Ile Gln Lys Gly Lys Asn Asn Gln Thr Glu Cys Phe Asn  
                                     100                                    105                                    110  
 Phe Ile Arg Phe Leu Gln Pro Tyr Asn Ala Ser His Leu Tyr Val Cys  
                                     115                                    120                                    125  
 Gly Thr Tyr Ala Phe Gln Pro Lys Cys Thr Tyr Val Asn Met Leu Thr  
                                     130                                    135                                    140  
 Phe Thr Leu Glu His Gly Glu Phe Glu Asp Gly Lys Gly Lys Cys Pro  
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 Tyr Asp Pro Ala Lys Gly His Ala Gly Leu Leu Val Asp Gly Glu Leu  
                                     165                                    170                                    175  
 Tyr Ser Ala Thr Leu Asn Asn Phe Leu Gly Thr Glu Pro Ile Ile Leu  
                                     180                                    185                                    190  
 Arg Asn Met Gly Pro His His Ser Met Lys Thr Glu Tyr Leu Ala Phe  
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 Trp Leu Asn Glu Pro His Phe Val Gly Ser Ala Tyr Val Pro Glu Ser  
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 Val Gly Ser Phe Thr Gly Asp Asp Asp Lys Val Tyr Phe Phe Phe Arg  
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 Glu Arg Ala Val Glu Ser Asp Cys Tyr Ala Glu Gln Val Val Ala Arg  
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 Val Ala Arg Val Cys Lys Gly Asp Met Gly Gly Ala Arg Thr Leu Gln  
                                     260                                    265                                    270  
 Arg Lys Trp Thr Thr Phe Leu Lys Ala Arg Leu Ala Cys Ser Ala Pro  
                                     275                                    280                                    285  
 Asn Trp Gln Leu Tyr Phe Asn Gln Leu Gln Ala Met His Thr Leu Gln  
                                     290                                    295                                    300  
 Asp Thr Ser Trp His Asn Thr Thr Phe Phe Gly Val Phe Gln Ala Gln  
                                     305                                    310                                    315                                    320  
 Trp Gly Asp Met Tyr Leu Ser Ala Ile Cys Glu Tyr Gln Leu Glu Glu  
                                     325                                    330                                    335  
 Ile Gln Arg Val Phe Glu Gly Pro Tyr Lys Glu Tyr His Glu Glu Ala  
                                     340                                    345                                    350  
 Gln Lys Trp Asp Arg Tyr Thr Asp Pro Val Pro Ser Pro Arg Pro Gly  
                                     355                                    360                                    365  
 Ser Cys Ile Asn Asn Trp His Arg Arg His Gly Tyr Thr Ser Ser Leu  
                                     370                                    375                                    380



Glu Leu Pro Asp Asn Ile Leu Asn Phe Val Lys Lys His Pro Leu Met  
 385 390 395 400  
 Glu Glu Gln Val Gly Pro Arg Trp Ser Arg Pro Leu Leu Val Lys Lys  
 405 410 415  
 Gly Thr Asn Phe Thr His Leu Val Ala Asp Arg Val Thr Gly Leu Asp  
 420 425 430  
 Gly Ala Thr Tyr Thr Val Leu Phe Ile Gly Thr Gly Asp Gly Trp Leu  
 435 440 445  
 Leu Lys Ala Val Ser Leu Gly Pro Trp Val His Leu Ile Glu Glu Leu  
 450 455 460  
 Gln Leu Phe Asp Gln Glu Pro Met Arg Ser Leu Val Leu Ser Gln Ser  
 465 470 475 480  
 Lys Lys Leu Leu Phe Ala Gly Ser Arg Ser Gln Leu Val Gln Leu Pro  
 485 490 495  
 Val Ala Asp Cys Ile Lys Tyr Arg Ser Cys Ala Asp Cys Val Leu Ala  
 500 505 510  
 Arg Asp Pro Tyr Cys Ala Trp Ser Val Asn Thr Ser Arg Cys Val Ala  
 515 520 525  
 Val Gly Gly His Phe Gly Ser Leu Leu Ile Gln His Val Met Thr Ser  
 530 535 540  
 Asp Thr Ser Gly Ile Cys Asn Leu Arg Gly Ser Lys Lys Val Arg Pro  
 545 550 555 560  
 Thr Pro Lys Asn Ile Thr Val Val Ala Gly Thr Asp Leu Val Leu Pro  
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 Cys His Leu Ser Ser Thr Trp Pro Arg Gly Ser Val Val Phe  
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accagcagga cagctggcct gaagctcaga gccggggcgt gcgcc atg gcc cca cac 177  
Met Ala Pro His

1

tgg gct gtc tgg ctg ctg gca gca agg ctg tgg ggc ctg ggc att ggg 225  
Trp Ala Val Trp Leu Leu Ala Ala Arg Leu Trp Gly Leu Gly Ile Gly  
5 10 15 20

gct gag gtg tgg tgg aac ctt gtg ccg cgt aag aca gtg tct tct ggg 273  
Ala Glu Val Trp Trp Asn Leu Val Pro Arg Lys Thr Val Ser Ser Gly  
25 30 35

gag ctg gcc acg gta gta cgg cgg ttc tcc cag acc ggc atc cag gac 321  
Glu Leu Ala Thr Val Val Arg Arg Phe Ser Gln Thr Gly Ile Gln Asp  
40 45 50

ttc ctg aca ctg acg ctg acg gag ccc act ggg ctt ctg tac gtg ggc 369  
Phe Leu Thr Leu Thr Leu Thr Glu Pro Thr Gly Leu Leu Tyr Val Gly  
55 60 65

gcc cga gag gcc ctg ttt gcc ttc agc atg gag gcc ctg gag ctg caa 417  
Ala Arg Glu Ala Leu Phe Ala Phe Ser Met Glu Ala Leu Glu Leu Gln  
70 75 80

gga gcg atc tcc tgg gag gcc ccc gtg gag aag aag act gag tgt atc 465  
Gly Ala Ile Ser Trp Glu Ala Pro Val Glu Lys Lys Thr Glu Cys Ile  
85 90 95 100

cag aaa ggg aag aac aac cag acc gag tgc ttc aac ttc atc cgc ttc 513  
Gln Lys Gly Lys Asn Asn Gln Thr Glu Cys Phe Asn Phe Ile Arg Phe  
105 110 115

ctg cag ccc tac aat gcc tcc cac ctg tac gtc tgt ggc acc tac gcc 561  
Leu Gln Pro Tyr Asn Ala Ser His Leu Tyr Val Cys Gly Thr Tyr Ala  
120 125 130

ttc cag ccc aag tgc acc tac gtc aac atg ctc acc ttc act ttg gag 609  
Phe Gln Pro Lys Cys Thr Tyr Val Asn Met Leu Thr Phe Thr Leu Glu  
135 140 145

cat gga gag ttt gaa gat ggg aag ggc aag tgt ccc tat gac cca gct 657  
His Gly Glu Phe Glu Asp Gly Lys Gly Lys Cys Pro Tyr Asp Pro Ala  
150 155 160

aag ggc cat gct ggc ctt ctt gtg gat ggt gag ctg tac tcg gcc aca 705  
Lys Gly His Ala Gly Leu Leu Val Asp Gly Glu Leu Tyr Ser Ala Thr  
165 170 175 180

ctc aac aac ttc ctg ggc acg gaa ccc att atc ctg cgt aac atg ggg 753  
Leu Asn Asn Phe Leu Gly Thr Glu Pro Ile Ile Leu Arg Asn Met Gly  
185 190 195

ccc cac cac tcc atg aag aca gag tac ctg gcc ttt tgg ctc aac gaa 801  
Pro His His Ser Met Lys Thr Glu Tyr Leu Ala Phe Trp Leu Asn Glu

200	205	210	
cct cac ttt gta ggc tct gcc tat gta cct gag agt gtg ggc agc ttc Pro His Phe Val Gly Ser Ala Tyr Val Pro Glu Ser Val Gly Ser Phe 215 220 225			849
acg ggg gac gac gac aag gtc tac ttc ttc ttc agg gag cgg gca gtg Thr Gly Asp Asp Asp Lys Val Tyr Phe Phe Phe Arg Glu Arg Ala Val 230 235 240			897
gag tcc gac tgc tat gcc gag cag gtg gtg gct cgt gtg gcc cgt gtc Glu Ser Asp Cys Tyr Ala Glu Gln Val Val Ala Arg Val Ala Arg Val 245 250 255 260			945
tgc aag ggc gat atg ggg ggc gca cgg acc ctg cag agg aag tgg acc Cys Lys Gly Asp Met Gly Gly Ala Arg Thr Leu Gln Arg Lys Trp Thr 265 270 275			993
acg ttc ctg aag gcg cgg ctg gca tgc tct gcc ccg aac tgg cag ctc Thr Phe Leu Lys Ala Arg Leu Ala Cys Ser Ala Pro Asn Trp Gln Leu 280 285 290			1041
tac ttc aac cag ctg cag gcg atg cac acc ctg cag gac acc tcc tgg Tyr Phe Asn Gln Leu Gln Ala Met His Thr Leu Gln Asp Thr Ser Trp 295 300 305			1089
cac aac acc acc ttc ttt ggg gtt ttt caa gca cag tgg ggt gac atg His Asn Thr Thr Phe Phe Gly Val Phe Gln Ala Gln Trp Gly Asp Met 310 315 320			1137
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aac tgg cat cgg cgc cac ggc tac acc agc tcc ctg gag cta ccc gac Asn Trp His Arg Arg His Gly Tyr Thr Ser Ser Leu Glu Leu Pro Asp 375 380 385			1329
aac atc ctc aac ttc gtc aag aag cac ccg ctg atg gag gag cag gtg Asn Ile Leu Asn Phe Val Lys Lys His Pro Leu Met Glu Glu Gln Val 390 395 400			1377
ggg cct cgg tgg agc cgc ccc ctg ctc gtg aag aag ggc acc aac ttc Gly Pro Arg Trp Ser Arg Pro Leu Leu Val Lys Lys Gly Thr Asn Phe 405 410 415 420			1425
acc cac ctg gtg gcc gac cgg gtt aca gga ctt gat gga gcc acc tat Thr His Leu Val Ala Asp Arg Val Thr Gly Leu Asp Gly Ala Thr Tyr 425 430 435			1473

aca gtg ctg ttc att ggc aca gga gac ggc tgg ctg ctc aag gct gtg 1521  
 Thr Val Leu Phe Ile Gly Thr Gly Asp Gly Trp Leu Leu Lys Ala Val  
 440 445 450  
 agc ctg ggg ccc tgg gtt cac ctg att gag gag ctg cag ctg ttt gac 1569  
 Ser Leu Gly Pro Trp Val His Leu Ile Glu Glu Leu Gln Leu Phe Asp  
 455 460 465  
 cag gag ccc atg aga agc ctg gtg cta tct cag agc aag aag ctg ctc 1617  
 Gln Glu Pro Met Arg Ser Leu Val Leu Ser Gln Ser Lys Lys Leu Leu  
 470 475 480  
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 Phe Ala Gly Ser Arg Ser Gln Leu Val Gln Leu Pro Val Ala Asp Cys  
 485 490 495 500  
 ata aag tat cgc tcc tgt gca gac tgt gtc ctc gcc cgg gac ccc tat 1713  
 Ile Lys Tyr Arg Ser Cys Ala Asp Cys Val Leu Ala Arg Asp Pro Tyr  
 505 510 515  
 tgc gcc tgg agc gtc aac acc agc cgc tgt gtg gcc gtg ggt ggc cac 1761  
 Cys Ala Trp Ser Val Asn Thr Ser Arg Cys Val Ala Val Gly Gly His  
 520 525 530  
 ttt gga tct tta ctg atc cag cat gtg atg acc tcg gac act tca ggc 1809  
 Phe Gly Ser Leu Leu Ile Gln His Val Met Thr Ser Asp Thr Ser Gly  
 535 540 545  
 att tgc aac ctc cgt ggc agt aag ata cag tca ggc cca ctn ccc aaa 1857  
 Ile Cys Asn Leu Arg Gly Ser Lys Ile Gln Ser Gly Pro Xaa Pro Lys  
 550 555 560  
 aac atc acg gtg gtg gcg ggc aca gac ctg gtg ctg ccc tgc cac ctc 1905  
 Asn Ile Thr Val Val Ala Gly Thr Asp Leu Val Leu Pro Cys His Leu  
 565 570 575 580  
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 585 590 595  
 tgaggggaac cccaccgcg tcggcggana gcgtgggagg tgtagctcct acttttgcac 2013  
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 ccagcaccca ccggccatg aggacctgct ctgctcagca cgggcactgc acttggtgtg 2133  
 gtcaccaggg caccagctcg cagaaggcat ctctctctc tctgtgaatc acagacacgc 2193  
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<213> Homo sapiens

<220>

<221> variation

<222> (562)

<223> Xaa may be any amino acid

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Val Ser Ser Gly Glu Leu Ala Thr Val Val Arg Arg Phe Ser Gln Thr  
35 40 45

Gly Ile Gln Asp Phe Leu Thr Leu Thr Leu Thr Glu Pro Thr Gly Leu  
50 55 60

Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Phe Ser Met Glu Ala  
65 70 75 80

Leu Glu Leu Gln Gly Ala Ile Ser Trp Glu Ala Pro Val Glu Lys Lys  
85 90 95

Thr Glu Cys Ile Gln Lys Gly Lys Asn Asn Gln Thr Glu Cys Phe Asn  
100 105 110

Phe Ile Arg Phe Leu Gln Pro Tyr Asn Ala Ser His Leu Tyr Val Cys  
115 120 125

Gly Thr Tyr Ala Phe Gln Pro Lys Cys Thr Tyr Val Asn Met Leu Thr  
130 135 140

Phe Thr Leu Glu His Gly Glu Phe Glu Asp Gly Lys Gly Lys Cys Pro  
145 150 155 160

Tyr Asp Pro Ala Lys Gly His Ala Gly Leu Leu Val Asp Gly Glu Leu  
165 170 175

Tyr Ser Ala Thr Leu Asn Asn Phe Leu Gly Thr Glu Pro Ile Ile Leu  
180 185 190

Arg Asn Met Gly Pro His His Ser Met Lys Thr Glu Tyr Leu Ala Phe  
195 200 205

Trp Leu Asn Glu Pro His Phe Val Gly Ser Ala Tyr Val Pro Glu Ser  
210 215 220

Val Gly Ser Phe Thr Gly Asp Asp Asp Lys Val Tyr Phe Phe Phe Arg  
225 230 235 240

Glu Arg Ala Val Glu Ser Asp Cys Tyr Ala Glu Gln Val Val Ala Arg  
245 250 255

Val Ala Arg Val Cys Lys Gly Asp Met Gly Gly Ala Arg Thr Leu Gln

260					265					270					
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	275						280					285			
Asn	Trp	Gln	Leu	Tyr	Phe	Asn	Gln	Leu	Gln	Ala	Met	His	Thr	Leu	Gln
	290					295					300				
Asp	Thr	Ser	Trp	His	Asn	Thr	Thr	Phe	Phe	Gly	Val	Phe	Gln	Ala	Gln
305					310					315					320
Trp	Gly	Asp	Met	Tyr	Leu	Ser	Ala	Ile	Cys	Glu	Tyr	Gln	Leu	Glu	Glu
				325					330					335	
Ile	Gln	Arg	Val	Phe	Glu	Gly	Pro	Tyr	Lys	Glu	Tyr	His	Glu	Glu	Ala
			340					345					350		
Gln	Lys	Trp	Asp	Arg	Tyr	Thr	Asp	Pro	Val	Pro	Ser	Pro	Arg	Pro	Gly
		355					360					365			
Ser	Cys	Ile	Asn	Asn	Trp	His	Arg	Arg	His	Gly	Tyr	Thr	Ser	Ser	Leu
	370					375					380				
Glu	Leu	Pro	Asp	Asn	Ile	Leu	Asn	Phe	Val	Lys	Lys	His	Pro	Leu	Met
385					390					395					400
Glu	Glu	Gln	Val	Gly	Pro	Arg	Trp	Ser	Arg	Pro	Leu	Leu	Val	Lys	Lys
				405					410					415	
Gly	Thr	Asn	Phe	Thr	His	Leu	Val	Ala	Asp	Arg	Val	Thr	Gly	Leu	Asp
			420					425					430		
Gly	Ala	Thr	Tyr	Thr	Val	Leu	Phe	Ile	Gly	Thr	Gly	Asp	Gly	Trp	Leu
		435					440					445			
Leu	Lys	Ala	Val	Ser	Leu	Gly	Pro	Trp	Val	His	Leu	Ile	Glu	Glu	Leu
	450					455					460				
Gln	Leu	Phe	Asp	Gln	Glu	Pro	Met	Arg	Ser	Leu	Val	Leu	Ser	Gln	Ser
465					470					475					480
Lys	Lys	Leu	Leu	Phe	Ala	Gly	Ser	Arg	Ser	Gln	Leu	Val	Gln	Leu	Pro
				485				490					495		
Val	Ala	Asp	Cys	Ile	Lys	Tyr	Arg	Ser	Cys	Ala	Asp	Cys	Val	Leu	Ala
			500					505					510		
Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Ser	Val	Asn	Thr	Ser	Arg	Cys	Val	Ala
		515					520					525			
Val	Gly	Gly	His	Phe	Gly	Ser	Leu	Leu	Ile	Gln	His	Val	Met	Thr	Ser
	530					535					540				
Asp	Thr	Ser	Gly	Ile	Cys	Asn	Leu	Arg	Gly	Ser	Lys	Ile	Gln	Ser	Gly
545					550					555					560
Pro	Xaa	Pro	Lys	Asn	Ile	Thr	Val	Val	Ala	Gly	Thr	Asp	Leu	Val	Leu

565 570 575  
 Pro Cys His Leu Ser Ser Asn Leu Ala Leu Pro Asp Ser Asn Pro Glu  
 580 585 590

Glu Ser Ser Val  
 595

<210> 15  
 <211> 1930  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (148)..(1755)

<220>  
 <221> variation  
 <222> (1)..(1930)  
 <223> N may be any nucleotide

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 ggggtgtggct gctccgccag ggtccccagg gtgggagagc ggctccgcgg ccaccgatgc 120  
 ccggaccccc tctgtcttct gctagac atg ctc ttc ctc tcg ttt cat gca ggc 174  
 Met Leu Phe Leu Ser Phe His Ala Gly  
 1 5

tct tgg gaa agc tgg tgc tgc tgc tgc ctg att ccc gcc gac aga cct 222  
 Ser Trp Glu Ser Trp Cys Cys Cys Cys Leu Ile Pro Ala Asp Arg Pro  
 10 15 20 25

tgg gac cgg ggc caa cac tgg cag ctg gag atg gcg gac acg aga tcc 270  
 Trp Asp Arg Gly Gln His Trp Gln Leu Glu Met Ala Asp Thr Arg Ser  
 30 35 40

gtg cac gag act agg ttt gag gcg gcc gtg aag gtg atc cag agt ttg 318  
 Val His Glu Thr Arg Phe Glu Ala Ala Val Lys Val Ile Gln Ser Leu  
 45 50 55

ccg aag aat ggt tca ttc cag cca aca aat gaa atg atg ctt aaa ttt 366  
 Pro Lys Asn Gly Ser Phe Gln Pro Thr Asn Glu Met Met Leu Lys Phe  
 60 65 70

tat agc ttc tat aag cag gca act gaa gga ccc tgt aaa ctt tca agg 414  
 Tyr Ser Phe Tyr Lys Gln Ala Thr Glu Gly Pro Cys Lys Leu Ser Arg  
 75 80 85

cct gga ttt tgg gat cct att gga aga tat aaa tgg gat gct tgg agt 462  
 Pro Gly Phe Trp Asp Pro Ile Gly Arg Tyr Lys Trp Asp Ala Trp Ser  
 90 95 100 105

tca ctg ggt gat atg acc aaa gag gaa gcc atg att gca tat gtt gaa 510

Ser	Leu	Gly	Asp	Met	Thr	Lys	Glu	Glu	Ala	Met	Ile	Ala	Tyr	Val	Glu		
				110					115					120			
gaa	atg	aaa	aag	att	att	gaa	act	atg	cca	atg	act	gag	aaa	gtt	gaa	558	
Glu	Met	Lys	Lys	Ile	Ile	Glu	Thr	Met	Pro	Met	Thr	Glu	Lys	Val	Glu		
			125					130					135				
gaa	ttg	ctg	cgt	gtc	ata	ggg	cca	ttt	tat	gaa	att	gtc	gag	gac	aaa	606	
Glu	Leu	Leu	Arg	Val	Ile	Gly	Pro	Phe	Tyr	Glu	Ile	Val	Glu	Asp	Lys		
			140				145					150					
aag	agt	ggc	agg	agt	tct	gat	ata	acc	tca	gtc	cga	ctg	gag	aaa	atc	654	
Lys	Ser	Gly	Arg	Ser	Ser	Asp	Ile	Thr	Ser	Val	Arg	Leu	Glu	Lys	Ile		
			155			160					165						
tct	aaa	tgt	tta	gaa	gat	ctt	ggg	aat	gtt	ctc	act	tct	act	cca	aac	702	
Ser	Lys	Cys	Leu	Glu	Asp	Leu	Gly	Asn	Val	Leu	Thr	Ser	Thr	Pro	Asn		
					175					180					185		
gcc	aaa	acc	gtt	aat	ggg	aaa	gct	gaa	agc	agt	gac	agt	gga	gcc	gag	750	
Ala	Lys	Thr	Val	Asn	Gly	Lys	Ala	Glu	Ser	Ser	Asp	Ser	Gly	Ala	Glu		
				190					195					200			
tct	gag	gaa	gaa	gag	gcc	caa	gaa	gaa	gtg	aaa	gga	gca	gaa	caa	agt	798	
Ser	Glu	Glu	Glu	Glu	Ala	Gln	Glu	Glu	Val	Lys	Gly	Ala	Glu	Gln	Ser		
				205				210					215				
gat	aat	gat	aag	aaa	atg	atg	aag	aag	tca	gca	gac	cat	aag	aat	ttg	846	
Asp	Asn	Asp	Lys	Lys	Met	Met	Lys	Lys	Ser	Ala	Asp	His	Lys	Asn	Leu		
			220				225					230					
gaa	gtc	att	gtc	act	aat	ggc	tat	gat	aaa	gat	ggc	ttt	gtt	cag	gat	894	
Glu	Val	Ile	Val	Thr	Asn	Gly	Tyr	Asp	Lys	Asp	Gly	Phe	Val	Gln	Asp		
			235			240					245						
ata	cag	aat	gac	att	cat	gcc	agt	tct	tcc	ctg	aat	ggc	aga	agc	act	942	
Ile	Gln	Asn	Asp	Ile	His	Ala	Ser	Ser	Ser	Leu	Asn	Gly	Arg	Ser	Thr		
					255					260					265		
gaa	gaa	gta	aag	ccc	att	gat	gaa	aac	ttg	ggg	caa	act	gga	aaa	tct	990	
Glu	Glu	Val	Lys	Pro	Ile	Asp	Glu	Asn	Leu	Gly	Gln	Thr	Gly	Lys	Ser		
				270				275						280			
gct	gtt	tgc	att	cac	caa	gat	ata	aat	gat	gat	cat	gtt	gaa	gat	gtt	1038	
Ala	Val	Cys	Ile	His	Gln	Asp	Ile	Asn	Asp	Asp	His	Val	Glu	Asp	Val		
				285				290					295				
aca	gga	att	cag	cat	ttg	aca	agc	gat	tca	gac	agt	gaa	gtt	tac	tgt	1086	
Thr	Gly	Ile	Gln	His	Leu	Thr	Ser	Asp	Ser	Asp	Ser	Glu	Val	Tyr	Cys		
				300			305					310					
gat	tct	atg	gaa	caa	ttt	gga	caa	gaa	gag	tct	tta	gac	agc	ttt	acg	1134	
Asp	Ser	Met	Glu	Gln	Phe	Gly	Gln	Glu	Glu	Ser	Leu	Asp	Ser	Phe	Thr		
						320					325						
tcc	aac	aat	gga	cca	ttt	cag	tat	tac	ttg	ggg	ggg	cat	tcc	agt	caa	1182	
Ser	Asn	Asn	Gly	Pro	Phe	Gln	Tyr	Tyr	Leu	Gly	Gly	His	Ser	Ser	Gln		



330	335	340	345	
ccc atg gaa aat tct gga ttt cgt gaa gat att caa gta cct cct gga				1230
Pro Met Glu Asn Ser Gly Phe Arg Glu Asp Ile Gln Val Pro Pro Gly				
	350	355	360	
aat ggc aac att ggg aat atg cag gtg gtt gca gtt gaa gga aaa ggt				1278
Asn Gly Asn Ile Gly Asn Met Gln Val Val Ala Val Glu Gly Lys Gly				
	365	370	375	
gaa gtc aag cat gga gga gaa gat ggc agg aat aac agc gga gca cca				1326
Glu Val Lys His Gly Gly Glu Asp Gly Arg Asn Asn Ser Gly Ala Pro				
	380	385	390	
cac cgg gag aag cga ggc gga gaa act gac gaa ttc tct aat gtt aga				1374
His Arg Glu Lys Arg Gly Gly Glu Thr Asp Glu Phe Ser Asn Val Arg				
	395	400	405	
aga gga aga gga cat agg atg caa cac ttg agc gaa gga acc aag ggc				1422
Arg Gly Arg Gly His Arg Met Gln His Leu Ser Glu Gly Thr Lys Gly				
	410	415	420	425
cgg cag gtg gga agt gga ggt gat ggg gag cgc tgg ggc tcc gac aga				1470
Arg Gln Val Gly Ser Gly Gly Asp Gly Glu Arg Trp Gly Ser Asp Arg				
	430	435	440	
ggg tcc cga ggc agc ctc aat gag cag atc gcc ctc gtg ctg atg aga				1518
Gly Ser Arg Gly Ser Leu Asn Glu Gln Ile Ala Leu Val Leu Met Arg				
	445	450	455	
ctg cag gag gac atg cag aat gtc ctt cag aga ctg cag aaa ctg gaa				1566
Leu Gln Glu Asp Met Gln Asn Val Leu Gln Arg Leu Gln Lys Leu Glu				
	460	465	470	
atg ctg act gct ttg cag gca aaa tca tca aca tca aca ttg cag act				1614
Met Leu Thr Ala Leu Gln Ala Lys Ser Ser Thr Ser Thr Leu Gln Thr				
	475	480	485	
gct cct cag ccc acc tca cag aga cca tct tgg tgg ccc ttc gag atg				1662
Ala Pro Gln Pro Thr Ser Gln Arg Pro Ser Trp Trp Pro Phe Glu Met				
	490	495	500	505
tct cct ggt gtg cta acg ttt gcc atc ata tgg cct ttt att gca cag				1710
Ser Pro Gly Val Leu Thr Phe Ala Ile Ile Trp Pro Phe Ile Ala Gln				
	510	515	520	
tgg ttg gtg tat tta tac tat caa aga agg aga aga aaa ctg aac				1755
Trp Leu Val Tyr Leu Tyr Tyr Gln Arg Arg Arg Lys Leu Asn				
	525	530	535	
tgagggaaaa tgggtgttttc ctcaagaaga ctactggaac tggatgacct cagaatgaac				1815
tggattgtgg tgttcacaag aaaatccttag tttgtgatga ttacattgct ttttgttgtc				1875
cngtagttta gtttgtgtac atatatacac atatataattt tgcactacac aaacg				1930

<210> 16  
 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<400> 16

Met	Leu	Phe	Leu	Ser	Phe	His	Ala	Gly	Ser	Trp	Glu	Ser	Trp	Cys	Cys
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Cys	Cys	Leu	Ile	Pro	Ala	Asp	Arg	Pro	Trp	Asp	Arg	Gly	Gln	His	Trp
			20					25					30		
Gln	Leu	Glu	Met	Ala	Asp	Thr	Arg	Ser	Val	His	Glu	Thr	Arg	Phe	Glu
		35					40					45			
Ala	Ala	Val	Lys	Val	Ile	Gln	Ser	Leu	Pro	Lys	Asn	Gly	Ser	Phe	Gln
		50				55					60				
Pro	Thr	Asn	Glu	Met	Met	Leu	Lys	Phe	Tyr	Ser	Phe	Tyr	Lys	Gln	Ala
	65				70					75					80
Thr	Glu	Gly	Pro	Cys	Lys	Leu	Ser	Arg	Pro	Gly	Phe	Trp	Asp	Pro	Ile
				85					90					95	
Gly	Arg	Tyr	Lys	Trp	Asp	Ala	Trp	Ser	Ser	Leu	Gly	Asp	Met	Thr	Lys
			100					105					110		
Glu	Glu	Ala	Met	Ile	Ala	Tyr	Val	Glu	Glu	Met	Lys	Lys	Ile	Ile	Glu
		115					120					125			
Thr	Met	Pro	Met	Thr	Glu	Lys	Val	Glu	Glu	Leu	Leu	Arg	Val	Ile	Gly
	130					135					140				
Pro	Phe	Tyr	Glu	Ile	Val	Glu	Asp	Lys	Lys	Ser	Gly	Arg	Ser	Ser	Asp
145					150					155					160
Ile	Thr	Ser	Val	Arg	Leu	Glu	Lys	Ile	Ser	Lys	Cys	Leu	Glu	Asp	Leu
				165					170					175	
Gly	Asn	Val	Leu	Thr	Ser	Thr	Pro	Asn	Ala	Lys	Thr	Val	Asn	Gly	Lys
		180						185					190		
Ala	Glu	Ser	Ser	Asp	Ser	Gly	Ala	Glu	Ser	Glu	Glu	Glu	Glu	Ala	Gln
		195					200					205			
Glu	Glu	Val	Lys	Gly	Ala	Glu	Gln	Ser	Asp	Asn	Asp	Lys	Lys	Met	Met
	210					215					220				
Lys	Lys	Ser	Ala	Asp	His	Lys	Asn	Leu	Glu	Val	Ile	Val	Thr	Asn	Gly
225					230					235					240
Tyr	Asp	Lys	Asp	Gly	Phe	Val	Gln	Asp	Ile	Gln	Asn	Asp	Ile	His	Ala
				245					250					255	
Ser	Ser	Ser	Leu	Asn	Gly	Arg	Ser	Thr	Glu	Glu	Val	Lys	Pro	Ile	Asp
			260					265					270		

Glu Asn Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln Asp  
 275 280 285  
 Ile Asn Asp Asp His Val Glu Asp Val Thr Gly Ile Gln His Leu Thr  
 290 295 300  
 Ser Asp Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly  
 305 310 315 320  
 Gln Glu Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln  
 325 330 335  
 Tyr Tyr Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser Gly Phe  
 340 345 350  
 Arg Glu Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly Asn Met  
 355 360 365  
 Gln Val Val Ala Val Glu Gly Lys Gly Glu Val Lys His Gly Gly Glu  
 370 375 380  
 Asp Gly Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg Gly Gly  
 385 390 395 400  
 Glu Thr Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met  
 405 410 415  
 Gln His Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly  
 420 425 430  
 Asp Gly Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn  
 435 440 445  
 Glu Gln Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp Met Gln Asn  
 450 455 460  
 Val Leu Gln Arg Leu Gln Lys Leu Glu Met Leu Thr Ala Leu Gln Ala  
 465 470 475 480  
 Lys Ser Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln  
 485 490 495  
 Arg Pro Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu Thr Phe  
 500 505 510  
 Ala Ile Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr Leu Tyr Tyr  
 515 520 525  
 Gln Arg Arg Arg Arg Lys Leu Asn  
 530 535

<210> 17  
 <211> 630  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS

<222> (123)..(623)

<400> 17

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caccttggac agagcgggtg cgcaaatcag aaggattagt tgggacctgc cttggcgacc 120

cc atg gca tcc ccc aga acc gta act att gtg gcc ctc tca gtg gcc 167  
Met Ala Ser Pro Arg Thr Val Thr Ile Val Ala Leu Ser Val Ala  
1 5 10 15

ctg gga ctc ttc ttt gtt ttc atg ggg act atc aag ctg acc ccc agg 215  
Leu Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro Arg  
20 25 30

ctc agc aag gat gcc tac agt gag atg aaa cgt gct tac aag agc tat 263  
Leu Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Tyr Lys Ser Tyr  
35 40 45

gtt cga gcc ctc cct ctg ctg aag aaa atg ggg atc aat tcc att ctc 311  
Val Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile Leu  
50 55 60

ctc cga aaa agc att ggt gcc ctt gaa gtg gcc tgt ggc atc gtc atg 359  
Leu Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met  
65 70 75

acc ctt gtg cct ggg cgt ccc aaa gat gtg gcc aac ttc ttc cta ctg 407  
Thr Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu  
80 85 90 95

ttg ctg gtg ttg gct gtg ctc ttc ttc cac cag ctg gtc ggt gat cct 455  
Leu Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro  
100 105 110

ctc aaa cgc tac gcc cat gct ctg gtg ttt gga atc ctg ctc act tgc 503  
Leu Lys Arg Tyr Ala His Ala Leu Val Phe Gly Ile Leu Leu Thr Cys  
115 120 125

cgc ctg ctg att gct cgc aag ccc gaa gac cgg tct tct gag aag aag 551  
Arg Leu Leu Ile Ala Arg Lys Pro Glu Asp Arg Ser Ser Glu Lys Lys  
130 135 140

cct ttg cca ggg aat gct gag gag caa ccc tcc tta tat gag aag gcc 599  
Pro Leu Pro Gly Asn Ala Glu Glu Gln Pro Ser Leu Tyr Glu Lys Ala  
145 150 155

cct cag ggc aaa gtg aag gtg tca tagaaaa 630  
Pro Gln Gly Lys Val Lys Val Ser  
160 165

<210> 18

<211> 167

<212> PRT

<213> Homo sapiens

<400> 18

Met Ala Ser Pro Arg Thr Val Thr Ile Val Ala Leu Ser Val Ala Leu  
1 5 10 15

Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro Arg Leu  
20 25 30

Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Tyr Lys Ser Tyr Val  
35 40 45

Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile Leu Leu  
50 55 60

Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met Thr  
65 70 75 80

Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu Leu  
85 90 95

Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro Leu  
100 105 110

Lys Arg Tyr Ala His Ala Leu Val Phe Gly Ile Leu Leu Thr Cys Arg  
115 120 125

Leu Leu Ile Ala Arg Lys Pro Glu Asp Arg Ser Ser Glu Lys Lys Pro  
130 135 140

Leu Pro Gly Asn Ala Glu Glu Gln Pro Ser Leu Tyr Glu Lys Ala Pro  
145 150 155 160

Gln Gly Lys Val Lys Val Ser  
165

<210> 19

<211> 1737

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (296)..(1687)

<220>

<221> variation

<222> (1)..(1737)

<223> N may be any nucleotide

<400> 19

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aaatcacccg tcttctgcgt cgctcacgct gggagctgta gaccagagct gttcctattc 120

ggccatcttg gctcctccct cgaaagatta tcactttgaa tatacggaa gtgatagcag 180

Q

195	200	205	
ata agg tgt aaa gac gac tct caa ttt tca gag gaa gga tcc agt gag Ile Arg Cys Lys Asp Asp Ser Gln Phe Ser Glu Glu Gly Ser Ser Glu 210 215 220 225			970
tgt aca gag cgc cct ccc tgt acc aca aaa gac tat ttc cag atc cat Cys Thr Glu Arg Pro Pro Cys Thr Thr Lys Asp Tyr Phe Gln Ile His 230 235 240			1018
act cca tgt gat gaa gaa gga aag aca cag ata atg tac aag tgg ata Thr Pro Cys Asp Glu Glu Gly Lys Thr Gln Ile Met Tyr Lys Trp Ile 245 250 255			1066
gag ccc aaa atc tgc cgg gag gat ctc aca gat gct att aga ttg ccc Glu Pro Lys Ile Cys Arg Glu Asp Leu Thr Asp Ala Ile Arg Leu Pro 260 265 270			1114
cct tct gga gag aag aag gat tgt ccg cct tgc aac cct gga ttt tat Pro Ser Gly Glu Lys Lys Asp Cys Pro Pro Cys Asn Pro Gly Phe Tyr 275 280 285			1162
aac aat gga tca tct tct tgc cat ccc tgt cct cct gga aca ttt tca Asn Asn Gly Ser Ser Ser Cys His Pro Cys Pro Pro Gly Thr Phe Ser 290 295 300 305			1210
gat gga acc aaa gaa tgt aga cca tgt cca gca gga acg gag cct gca Asp Gly Thr Lys Glu Cys Arg Pro Cys Pro Ala Gly Thr Glu Pro Ala 310 315 320			1258
ctt ggc ttt gaa tat aaa tgg tgg aat gtc ctt cct ggc aac atg aaa Leu Gly Phe Glu Tyr Lys Trp Trp Asn Val Leu Pro Gly Asn Met Lys 325 330 335			1306
act tcc tgc ttc aat gtt ggg aat tca aag tgc gat gga atg aat ggt Thr Ser Cys Phe Asn Val Gly Asn Ser Lys Cys Asp Gly Met Asn Gly 340 345 350			1354
tgg gag gtg gct gga gat cat atc cag agt ggg gct gga ggt tct gac Trp Glu Val Ala Gly Asp His Ile Gln Ser Gly Ala Gly Gly Ser Asp 355 360 365			1402
aat gat tac ctg atc tta aac ttg cat atc cca gga ttt aaa cca cca Asn Asp Tyr Leu Ile Leu Asn Leu His Ile Pro Gly Phe Lys Pro Pro 370 375 380 385			1450
aca tct atg act gga gcc acg ggt tct gaa cta gga aga ata aca ttt Thr Ser Met Thr Gly Ala Thr Gly Ser Glu Leu Gly Arg Ile Thr Phe 390 395 400			1498
gtc ttt gag acc ctc tgt tca gct gac tgt gtt ttg tac ttc atg gtg Val Phe Glu Thr Leu Cys Ser Ala Asp Cys Val Leu Tyr Phe Met Val 405 410 415			1546
gat att aat aga aaa agt aca aat gtg gta gaa tcg tgg ggt gga acc Asp Ile Asn Arg Lys Ser Thr Asn Val Val Glu Ser Trp Gly Gly Thr 420 425 430			1594

aaa gaa aaa caa gct tac acc cat atc atc ttc aag aat gca act ttt 1642  
 Lys Glu Lys Gln Ala Tyr Thr His Ile Ile Phe Lys Asn Ala Thr Phe  
 435 440 445

aca ttt aca tgg ggc att ccc aga gaa cta att cag ggt cca aga 1687  
 Thr Phe Thr Trp Gly Ile Pro Arg Glu Leu Ile Gln Gly Pro Arg  
 450 455 460

taatagacgg ttccnccatt gacatgtttg aaggatttat tcctattcac 1737

<210> 20  
 <211> 464  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Met Lys Asn Gln Val Cys Ser Lys Cys Gly Glu Gly Thr Tyr Ser Leu  
 1 5 10 15

Gly Ser Gly Ile Lys Phe Asp Glu Trp Asp Glu Leu Pro Ala Gly Phe  
 20 25 30

Ser Asn Ile Ala Thr Phe Met Asp Thr Val Val Gly Pro Ser Asp Ser  
 35 40 45

Arg Pro Asp Gly Cys Asn Asn Ser Ser Trp Ile Pro Arg Gly Asn Tyr  
 50 55 60

Ile Glu Ser Asn Arg Asp Asp Cys Thr Val Ser Leu Ile Tyr Ala Val  
 65 70 75 80

His Leu Lys Lys Ser Gly Tyr Val Phe Phe Glu Tyr Gln Tyr Val Asp  
 85 90 95

Asn Asn Ile Phe Phe Glu Phe Phe Ile Gln Asn Asp Gln Cys Gln Glu  
 100 105 110

Met Asp Thr Thr Thr Asp Lys Trp Val Lys Leu Thr Asp Asn Gly Glu  
 115 120 125

Trp Gly Ser His Ser Val Met Leu Lys Ser Gly Thr Asn Ile Leu Tyr  
 130 135 140

Trp Arg Thr Thr Gly Ile Leu Met Gly Ser Lys Ala Val Lys Pro Val  
 145 150 155 160

Leu Val Lys Asn Ile Thr Ile Glu Gly Val Ala Tyr Thr Ser Glu Cys  
 165 170 175

Phe Pro Cys Lys Pro Gly Thr Phe Ser Asn Lys Pro Gly Ser Phe Asn  
 180 185 190

Cys Gln Val Cys Pro Arg Asn Thr Tyr Ser Glu Lys Gly Ala Lys Glu  
 195 200 205



Cys Ile Arg Cys Lys Asp Asp Ser Gln Phe Ser Glu Glu Gly Ser Ser  
 210 215 220  
 Glu Cys Thr Glu Arg Pro Pro Cys Thr Thr Lys Asp Tyr Phe Gln Ile  
 225 230 235 240  
 His Thr Pro Cys Asp Glu Glu Gly Lys Thr Gln Ile Met Tyr Lys Trp  
 245 250 255  
 Ile Glu Pro Lys Ile Cys Arg Glu Asp Leu Thr Asp Ala Ile Arg Leu  
 260 265 270  
 Pro Pro Ser Gly Glu Lys Lys Asp Cys Pro Pro Cys Asn Pro Gly Phe  
 275 280 285  
 Tyr Asn Asn Gly Ser Ser Ser Cys His Pro Cys Pro Pro Gly Thr Phe  
 290 295 300  
 Ser Asp Gly Thr Lys Glu Cys Arg Pro Cys Pro Ala Gly Thr Glu Pro  
 305 310 315 320  
 Ala Leu Gly Phe Glu Tyr Lys Trp Trp Asn Val Leu Pro Gly Asn Met  
 325 330 335  
 Lys Thr Ser Cys Phe Asn Val Gly Asn Ser Lys Cys Asp Gly Met Asn  
 340 345 350  
 Gly Trp Glu Val Ala Gly Asp His Ile Gln Ser Gly Ala Gly Gly Ser  
 355 360 365  
 Asp Asn Asp Tyr Leu Ile Leu Asn Leu His Ile Pro Gly Phe Lys Pro  
 370 375 380  
 Pro Thr Ser Met Thr Gly Ala Thr Gly Ser Glu Leu Gly Arg Ile Thr  
 385 390 395 400  
 Phe Val Phe Glu Thr Leu Cys Ser Ala Asp Cys Val Leu Tyr Phe Met  
 405 410 415  
 Val Asp Ile Asn Arg Lys Ser Thr Asn Val Val Glu Ser Trp Gly Gly  
 420 425 430  
 Thr Lys Glu Lys Gln Ala Tyr Thr His Ile Ile Phe Lys Asn Ala Thr  
 435 440 445  
 Phe Thr Phe Thr Trp Gly Ile Pro Arg Glu Leu Ile Gln Gly Pro Arg  
 450 455 460

<210> 21  
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 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (166)..(2037)

<220>  
 <221> variation  
 <222> (1)..(2156)  
 <223> N may be any nucleotide

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attgtctgcg ctggggaagg ggacaggccg ggaccgggac ctccgctcgc agccggccgc 120

accagcagga cagctggcct gaagctcaga gccggggcgt gcgcc atg gcc cca cac 177  
 Met Ala Pro His

1

tgg gct gtc tgg ctg ctg gca gca agg ctg tgg ggc ctg ggc att ggg 225  
 Trp Ala Val Trp Leu Leu Ala Ala Arg Leu Trp Gly Leu Gly Ile Gly  
 5 10 15 20

gct gag gtg tgg tgg aac ctt gtg ccg cgt aag aca gtg tct tct ggg 273  
 Ala Glu Val Trp Trp Asn Leu Val Pro Arg Lys Thr Val Ser Ser Gly  
 25 30 35

gag ctg gcc acg gta gta cgg cgg ttc tcc cag acc ggc atc cag gac 321  
 Glu Leu Ala Thr Val Val Arg Arg Phe Ser Gln Thr Gly Ile Gln Asp  
 40 45 50

ttc ctg aca ctg acg ctg acg gag ccc act ggg ctt ctg tac gtg ggc 369  
 Phe Leu Thr Leu Thr Leu Thr Glu Pro Thr Gly Leu Leu Tyr Val Gly  
 55 60 65

gcc cga gag gcc ctg ttt gcc ttc agc atg gag gcc ctg gag ctg caa 417  
 Ala Arg Glu Ala Leu Phe Ala Phe Ser Met Glu Ala Leu Glu Leu Gln  
 70 75 80

gga gcg atc tcc tgg gag gcc ccc gtg gag aag aag act gag tgt atc 465  
 Gly Ala Ile Ser Trp Glu Ala Pro Val Glu Lys Lys Thr Glu Cys Ile  
 85 90 95 100

cag aaa ggg aag aac aac cag acc gag tgc ttc aac ttc atc cgc ttc 513  
 Gln Lys Gly Lys Asn Asn Gln Thr Glu Cys Phe Asn Phe Ile Arg Phe  
 105 110 115

ctg cag ccc tac aat gcc tcc cac ctg tac gtc tgt ggc acc tac gcc 561  
 Leu Gln Pro Tyr Asn Ala Ser His Leu Tyr Val Cys Gly Thr Tyr Ala  
 120 125 130

ttc cag ccc aag tgc acc tac gtc aac atg ctc acc ttc act ttg gag 609  
 Phe Gln Pro Lys Cys Thr Tyr Val Asn Met Leu Thr Phe Thr Leu Glu  
 135 140 145

cat gga gag ttt gaa gat ggg aag ggc aag tgt ccc tat gac cca gct 657  
 His Gly Glu Phe Glu Asp Gly Lys Gly Lys Cys Pro Tyr Asp Pro Ala  
 150 155 160

aag ggc cat gct ggc ctt ctt gtg gat ggt gag ctg tac tcg gcc aca 705  
 Lys Gly His Ala Gly Leu Leu Val Asp Gly Glu Leu Tyr Ser Ala Thr

165	170	175	180	
ctc aac aac ttc ctg ggc acg gaa ccc att atc ctg cgt aac atg ggg				753
Leu Asn Asn Phe Leu Gly Thr Glu Pro Ile Ile Leu Arg Asn Met Gly				
	185	190	195	
ccc cac cac tcc atg aag aca gag tac ctg gcc ttt tgg ctc aac gaa				801
Pro His His Ser Met Lys Thr Glu Tyr Leu Ala Phe Trp Leu Asn Glu				
	200	205	210	
cct cac ttt gta ggc tct gcc tat gta cct gag agt gtg ggc agc ttc				849
Pro His Phe Val Gly Ser Ala Tyr Val Pro Glu Ser Val Gly Ser Phe				
	215	220	225	
acg ggg gac gac gac aag gtc tac ttc ttc ttc agg gag cgg gca gtg				897
Thr Gly Asp Asp Asp Lys Val Tyr Phe Phe Phe Arg Glu Arg Ala Val				
	230	235	240	
gag tcc gac tgc tat gcc gag cag gtg gtg gct cgt gtg gcc cgt gtc				945
Glu Ser Asp Cys Tyr Ala Glu Gln Val Val Ala Arg Val Ala Arg Val				
	245	250	255	260
tgc aag ggc gat atg ggg ggc gca cgg acc ctg cag agg aag tgg acc				993
Cys Lys Gly Asp Met Gly Gly Ala Arg Thr Leu Gln Arg Lys Trp Thr				
	265	270	275	
acg ttc ctg aag gcg cgg ctg gca tgc tct gcc ccg aac tgg cag ctc				1041
Thr Phe Leu Lys Ala Arg Leu Ala Cys Ser Ala Pro Asn Trp Gln Leu				
	280	285	290	
tac ttc aac cag ctg cag gcg atg cac acc ctg cag gac acc tcc tgg				1089
Tyr Phe Asn Gln Leu Gln Ala Met His Thr Leu Gln Asp Thr Ser Trp				
	295	300	305	
cac aac acc acc ttc ttt ggg gtt ttt caa gca cag tgg ggt gac atg				1137
His Asn Thr Thr Phe Phe Gly Val Phe Gln Ala Gln Trp Gly Asp Met				
	310	315	320	
tac ctg tcg gcc atc tgt gag tac cag ttg gaa gag atc cag cgg gtg				1185
Tyr Leu Ser Ala Ile Cys Glu Tyr Gln Leu Glu Glu Ile Gln Arg Val				
	325	330	335	340
ttt gag ggc ccc tat aag gag tac cat gag gaa gcc cag aag tgg gac				1233
Phe Glu Gly Pro Tyr Lys Glu Tyr His Glu Glu Ala Gln Lys Trp Asp				
	345	350	355	
cgc tac act gac cct gta ccc agc cct cgg cct ggc tcg tgc att aac				1281
Arg Tyr Thr Asp Pro Val Pro Ser Pro Arg Pro Gly Ser Cys Ile Asn				
	360	365	370	
aac tgg cat cgg cgc cac ggc tac acc agc tcc ctg gag cta ccc gac				1329
Asn Trp His Arg Arg His Gly Tyr Thr Ser Ser Leu Glu Leu Pro Asp				
	375	380	385	
aac atc ctc aac ttc gtc aag aag cac ccg ctg atg gag gag cag gtg				1377
Asn Ile Leu Asn Phe Val Lys Lys His Pro Leu Met Glu Glu Gln Val				
	390	395	400	

ggg cct cgg tgg agc cgc ccc ctg ctc gtg aag aag ggc acc aac ttc 1425  
 Gly Pro Arg Trp Ser Arg Pro Leu Leu Val Lys Lys Gly Thr Asn Phe  
 405 410 415 420

acc cac ctg gtg gcc gac cgg gtt aca gga ctt gat gga gcc acc tat 1473  
 Thr His Leu Val Ala Asp Arg Val Thr Gly Leu Asp Gly Ala Thr Tyr  
 425 430 435

aca gtg ctg ttc att ggc aca gga gac ggc tgg ctg ctc aag gct gtg 1521  
 Thr Val Leu Phe Ile Gly Thr Gly Asp Gly Trp Leu Leu Lys Ala Val  
 440 445 450

agc ctg ggg ccc tgg gtt cac ctg att gag gag ctg cag ctg ttt gac 1569  
 Ser Leu Gly Pro Trp Val His Leu Ile Glu Glu Leu Gln Leu Phe Asp  
 455 460 465

cag gag ccc atg aga agc ctg gtg cta tct cag agc aaa aag ctg ctc 1617  
 Gln Glu Pro Met Arg Ser Leu Val Leu Ser Gln Ser Lys Lys Leu Leu  
 470 475 480

ttt gcc ggc tcc cgc tct cag ctg gtg cag ctg ccc gtg gcc gac tgc 1665  
 Phe Ala Gly Ser Arg Ser Gln Leu Val Gln Leu Pro Val Ala Asp Cys  
 485 490 495 500

att aag tat cgc tcc tgt gca gac tgt gtc ctc gcc cgg gac ccc tat 1713  
 Ile Lys Tyr Arg Ser Cys Ala Asp Cys Val Leu Ala Arg Asp Pro Tyr  
 505 510 515

tgc gcc tgg agc gtc aac acc agc cgc tgt gtg gcc gtg ggt ggc cac 1761  
 Cys Ala Trp Ser Val Asn Thr Ser Arg Cys Val Ala Val Gly Gly His  
 520 525 530

tct gga tct cta ctg atc cag cat gtg atg acc tcg gac act tca ggc 1809  
 Ser Gly Ser Leu Leu Ile Gln His Val Met Thr Ser Asp Thr Ser Gly  
 535 540 545

atc tgc aac ctc cgt ggc agt aag aaa gtc agg ccc act ccc aaa aac 1857  
 Ile Cys Asn Leu Arg Gly Ser Lys Lys Val Arg Pro Thr Pro Lys Asn  
 550 555 560

atc acg gtg gtg gcg ggc aca gac ctg gtg ctg ccc tgc cac ctc tcc 1905  
 Ile Thr Val Val Ala Gly Thr Asp Leu Val Leu Pro Cys His Leu Ser  
 565 570 575 580

tcc act tgg ccc cgg ggt tca gtg gta ttt tat act tgc ctt ctt cct 1953  
 Ser Thr Trp Pro Arg Gly Ser Val Val Phe Tyr Thr Cys Leu Leu Pro  
 585 590 595

gta cag ggc tgg gaa agg ctg tgt gag ggg aaa aaa agg aaa ggg tgg 2001  
 Val Gln Gly Trp Glu Arg Leu Cys Glu Gly Lys Lys Arg Lys Gly Trp  
 600 605 610

gcc tgc tgt gga caa tgg cat act ctc ttc cag ccc taggaggagg 2047  
 Ala Cys Cys Gly Gln Trp His Thr Leu Phe Gln Pro  
 615 620

gctcctaaca gtgtaactta ttgtgtcccc gcgtatttat ttgttgtaaa tatttgagta 2107  
 tttttatatt gacaaataaa atggagaaaa tgaaaaaaaa aaaaaaaaaa 2156

<210> 22  
 <211> 624  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
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 Leu Gly Ile Gly Ala Glu Val Trp Trp Asn Leu Val Pro Arg Lys Thr  
 20 25 30  
 Val Ser Ser Gly Glu Leu Ala Thr Val Val Arg Arg Phe Ser Gln Thr  
 35 40 45  
 Gly Ile Gln Asp Phe Leu Thr Leu Thr Leu Thr Glu Pro Thr Gly Leu  
 50 55 60  
 Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Phe Ser Met Glu Ala  
 65 70 75 80  
 Leu Glu Leu Gln Gly Ala Ile Ser Trp Glu Ala Pro Val Glu Lys Lys  
 85 90 95  
 Thr Glu Cys Ile Gln Lys Gly Lys Asn Asn Gln Thr Glu Cys Phe Asn  
 100 105 110  
 Phe Ile Arg Phe Leu Gln Pro Tyr Asn Ala Ser His Leu Tyr Val Cys  
 115 120 125  
 Gly Thr Tyr Ala Phe Gln Pro Lys Cys Thr Tyr Val Asn Met Leu Thr  
 130 135 140  
 Phe Thr Leu Glu His Gly Glu Phe Glu Asp Gly Lys Gly Lys Cys Pro  
 145 150 155 160  
 Tyr Asp Pro Ala Lys Gly His Ala Gly Leu Leu Val Asp Gly Glu Leu  
 165 170 175  
 Tyr Ser Ala Thr Leu Asn Asn Phe Leu Gly Thr Glu Pro Ile Ile Leu  
 180 185 190  
 Arg Asn Met Gly Pro His His Ser Met Lys Thr Glu Tyr Leu Ala Phe  
 195 200 205  
 Trp Leu Asn Glu Pro His Phe Val Gly Ser Ala Tyr Val Pro Glu Ser  
 210 215 220  
 Val Gly Ser Phe Thr Gly Asp Asp Asp Lys Val Tyr Phe Phe Phe Arg  
 225 230 235 240  
 Glu Arg Ala Val Glu Ser Asp Cys Tyr Ala Glu Gln Val Val Ala Arg

245                      250                      255  
 Val Ala Arg Val Cys Lys Gly Asp Met Gly Gly Ala Arg Thr Leu Gln  
                                  260                      265                      270  
 Arg Lys Trp Thr Thr Phe Leu Lys Ala Arg Leu Ala Cys Ser Ala Pro  
                                  275                      280                      285  
 Asn Trp Gln Leu Tyr Phe Asn Gln Leu Gln Ala Met His Thr Leu Gln  
                                  290                      295                      300  
 Asp Thr Ser Trp His Asn Thr Thr Phe Phe Gly Val Phe Gln Ala Gln  
 305                                   310                                   315                                   320  
 Trp Gly Asp Met Tyr Leu Ser Ala Ile Cys Glu Tyr Gln Leu Glu Glu  
                                  325                                   330                                   335  
 Ile Gln Arg Val Phe Glu Gly Pro Tyr Lys Glu Tyr His Glu Glu Ala  
                                  340                                   345                                   350  
 Gln Lys Trp Asp Arg Tyr Thr Asp Pro Val Pro Ser Pro Arg Pro Gly  
                                  355                                   360                                   365  
 Ser Cys Ile Asn Asn Trp His Arg Arg His Gly Tyr Thr Ser Ser Leu  
                                  370                                   375                                   380  
 Glu Leu Pro Asp Asn Ile Leu Asn Phe Val Lys Lys His Pro Leu Met  
 385                                   390                                   395                                   400  
 Glu Glu Gln Val Gly Pro Arg Trp Ser Arg Pro Leu Leu Val Lys Lys  
                                  405                                   410                                   415  
 Gly Thr Asn Phe Thr His Leu Val Ala Asp Arg Val Thr Gly Leu Asp  
                                  420                                   425                                   430  
 Gly Ala Thr Tyr Thr Val Leu Phe Ile Gly Thr Gly Asp Gly Trp Leu  
                                  435                                   440                                   445  
 Leu Lys Ala Val Ser Leu Gly Pro Trp Val His Leu Ile Glu Glu Leu  
                                  450                                   455                                   460  
 Gln Leu Phe Asp Gln Glu Pro Met Arg Ser Leu Val Leu Ser Gln Ser  
 465                                   470                                   475                                   480  
 Lys Lys Leu Leu Phe Ala Gly Ser Arg Ser Gln Leu Val Gln Leu Pro  
                                  485                                   490                                   495  
 Val Ala Asp Cys Ile Lys Tyr Arg Ser Cys Ala Asp Cys Val Leu Ala  
                                  500                                   505                                   510  
 Arg Asp Pro Tyr Cys Ala Trp Ser Val Asn Thr Ser Arg Cys Val Ala  
                                  515                                   520                                   525  
 Val Gly Gly His Ser Gly Ser Leu Leu Ile Gln His Val Met Thr Ser  
                                  530                                   535                                   540  
 Asp Thr Ser Gly Ile Cys Asn Leu Arg Gly Ser Lys Lys Val Arg Pro

545		550		555		560
Thr Pro Lys Asn Ile Thr Val Val Ala Gly Thr Asp Leu Val Leu Pro						
	565			570		575
Cys His Leu Ser Ser Thr Trp Pro Arg Gly Ser Val Val Phe Tyr Thr						
	580		585			590
Cys Leu Leu Pro Val Gln Gly Trp Glu Arg Leu Cys Glu Gly Lys Lys						
	595		600			605
Arg Lys Gly Trp Ala Cys Cys Gly Gln Trp His Thr Leu Phe Gln Pro						
	610		615		620	

<210> 23  
 <211> 2056  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (7)..(1608)

<220>  
 <221> variation  
 <222> (1)..(2056)  
 <223> N may be any nucleotide

<220>  
 <221> variation  
 <222> (1)..(2056)  
 <223> N may be any nucleotide

<400> 23  
 cgctcc atg tat nag ttt cat gca ggc tct tgg gaa agc tgg tgc tgc 48  
 Met Tyr Xaa Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys  
 1 5 10

tgc tgc ctg att ccc gcc gac aga cct tgg gac cgg ggc caa cac tgg 96  
 Cys Cys Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp  
 15 20 25 30

cag ctg gag atg gcg gac acg aga tcc gtg cac gag act agg ttt gag 144  
 Gln Leu Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu  
 35 40 45

gcg gcc gtg aag gtg atc cag agt ttg ccg aag aat gat tca ttc cag 192  
 Ala Ala Val Lys Val Ile Gln Ser Leu Pro Lys Asn Asp Ser Phe Gln  
 50 55 60

cca aca aat gaa atg atg ctt aaa ttt tat agc ttc tat aag cag gca 240  
 Pro Thr Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala  
 65 70 75

act gaa gga ccc tgt aaa ctt tca agg cct gga ttt tgg gat cct att 288  
 Thr Glu Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile

80	85	90	
gga aga tat aaa tgg gat gct tgg agt tca ctg ggt gat atg acc aaa			336
Gly Arg Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys			
95	100	105	110
gag gaa gcc atg att gca tat gtt gaa gaa atg aaa aag att att gaa			384
Glu Glu Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu			
	115	120	125
act atg cca atg act gag aaa gtt gaa gaa ttg ctg cgt gtc ata ggt			432
Thr Met Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly			
	130	135	140
cca ttt tat gaa att gtc gag gac aaa aag agt ggc agg agt tct gat			480
Pro Phe Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp			
	145	150	155
ata acc tca gtc cga ctg gag aaa atc tct aaa tgt tta gaa gat ctt			528
Ile Thr Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu			
	160	165	170
ggt aat gtt ctc act tct act cca aac gcc aaa acc gtt aat ggt aaa			576
Gly Asn Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys			
175	180	185	190
gct gaa agc agt gac agt gga gcc gag tct gag gaa gaa gag gcc caa			624
Ala Glu Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Glu Ala Gln			
	195	200	205
gaa gaa gtg aaa gga gca gaa caa agt gat aat gat aag aaa atg atg			672
Glu Glu Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met			
	210	215	220
aag aag tca gca gac cat aag aat ttg gaa gtc att gtc act aat ggc			720
Lys Lys Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly			
	225	230	235
tat gat aaa gat ggc ttt gtt cag gat ata cag aat gac att cat gcc			768
Tyr Asp Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala			
	240	245	250
agt tct tcc ctg aat ggc aga agc act gaa gaa gta aag ccc att gat			816
Ser Ser Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp			
255	260	265	270
gaa aac ttg ggg caa act gga aaa tct gct gtt tgc att cac caa gat			864
Glu Asn Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln Asp			
	275	280	285
ata aat gat gat cat gtt gaa gat gtt aca gga att cag cat ttg aca			912
Ile Asn Asp Asp His Val Glu Asp Val Thr Gly Ile Gln His Leu Thr			
	290	295	300
agc gat tca gac agt gaa gtt tac tgt gat tct atg gaa caa ttt gga			960
Ser Asp Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly			
	305	310	315



caa gaa gag tct tta gac agc ttt acg tcc aac aat gga cca ttt cag	1008
Gln Glu Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln	
320 325 330	
tat tac ttg ggt ggt cat tcc agt caa ccc atg gaa aat tct gga ttt	1056
Tyr Tyr Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser Gly Phe	
335 340 345 350	
cgt gaa gat att caa gta cct cct gga aat ggc aac att ggg aat atg	1104
Arg Glu Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly Asn Met	
355 360 365	
cag gtg gtt gca gtt gaa gga aaa ggt gaa gtc aag cat gga gga gaa	1152
Gln Val Val Ala Val Glu Gly Lys Gly Glu Val Lys His Gly Gly Glu	
370 375 380	
gat ggc agg aat aac agc gga gca cca cac cgg gag aag cga ggc gga	1200
Asp Gly Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg Gly Gly	
385 390 395	
gaa act gac gaa ttc tct aat gtt aga aga gga aga gga cat agg atg	1248
Glu Thr Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met	
400 405 410	
caa cac ttg agc gaa gga acc aag ggc cgg cag gtg gga agt gga ggt	1296
Gln His Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly	
415 420 425 430	
gat ggg gag cgc tgg ggc tcc gac aga ggg tcc cga ggc agc ctc aat	1344
Asp Gly Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn	
435 440 445	
gag cag atc gcc ctc gtg ctg atg aga ctg cag gag gac atg cag aat	1392
Glu Gln Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp Met Gln Asn	
450 455 460	
gtc ctt cag aga ctg cag aaa ctg gaa acg ctg act gct ttg cag gca	1440
Val Leu Gln Arg Leu Gln Lys Leu Glu Thr Leu Thr Ala Leu Gln Ala	
465 470 475	
aaa tca tca aca tca aca ttg cag act gct cct cag ccc acc tca cag	1488
Lys Ser Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln	
480 485 490	
aga cca tct tgg tgg ccc ttc gag atg tct cct ggt gtg cta acg ttt	1536
Arg Pro Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu Thr Phe	
495 500 505 510	
gcc atc ata tgg cct ttt att gca cag tgg ttg gtg tat tta tac tat	1584
Ala Ile Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr Leu Tyr Tyr	
515 520 525	
caa aga agg aga aga aaa ctg aac tgaggaaaat ggtgttttcc tcaagaagac	1638
Gln Arg Arg Arg Arg Lys Leu Asn	
530	

tactggaact ggatgacctc agaatgaact ggattgtggt gttcacaaga aaatccttagt 1698  
 ttgtgatgat tacattgctt tttgttgctc agtagtttag tttgtgtaca tatatacaca 1758  
 tatatatattt gcactacaca aacgataaca ttttaaggac taatattgct gatacttgaa 1818  
 taatcaatct ctactagggtt ataagtagta tacacagatt taccctgccc ttgaacttga 1878  
 aggacattaa attattaatg atcatttggt aacatgttta cctgattatc ttccatagag 1938  
 taacataagc tgcttttcaa aggtaccatt gtgataatga gatcaaattt ataagttatt 1998  
 atttttaatt ttctaaatta aataaaagaa agaatgcaaa aaaaaaaaaa aaaaaaaaaa 2056

<210> 24  
 <211> 534  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> variation  
 <222> (3)  
 <223> Xaa may be any amino acid

<400> 24  
 Met Tyr Xaa Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys Cys Cys  
 1 5 10 15  
 Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp Gln Leu  
 20 25 30  
 Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala  
 35 40 45  
 Val Lys Val Ile Gln Ser Leu Pro Lys Asn Asp Ser Phe Gln Pro Thr  
 50 55 60  
 Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu  
 65 70 75 80  
 Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg  
 85 90 95  
 Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu  
 100 105 110  
 Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met  
 115 120 125  
 Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe  
 130 135 140  
 Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr  
 145 150 155 160  
 Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu Gly Asn

165										170					175				
Val	Leu	Thr	Ser	Thr	Pro	Asn	Ala	Lys	Thr	Val	Asn	Gly	Lys	Ala	Glu				
			180					185					190						
Ser	Ser	Asp	Ser	Gly	Ala	Glu	Ser	Glu	Glu	Glu	Glu	Ala	Gln	Glu	Glu				
		195					200					205							
Val	Lys	Gly	Ala	Glu	Gln	Ser	Asp	Asn	Asp	Lys	Lys	Met	Met	Lys	Lys				
	210					215					220								
Ser	Ala	Asp	His	Lys	Asn	Leu	Glu	Val	Ile	Val	Thr	Asn	Gly	Tyr	Asp				
225					230				235					240					
Lys	Asp	Gly	Phe	Val	Gln	Asp	Ile	Gln	Asn	Asp	Ile	His	Ala	Ser	Ser				
			245					250						255					
Ser	Leu	Asn	Gly	Arg	Ser	Thr	Glu	Glu	Val	Lys	Pro	Ile	Asp	Glu	Asn				
		260						265					270						
Leu	Gly	Gln	Thr	Gly	Lys	Ser	Ala	Val	Cys	Ile	His	Gln	Asp	Ile	Asn				
	275						280					285							
Asp	Asp	His	Val	Glu	Asp	Val	Thr	Gly	Ile	Gln	His	Leu	Thr	Ser	Asp				
290						295			300										
Ser	Asp	Ser	Glu	Val	Tyr	Cys	Asp	Ser	Met	Glu	Gln	Phe	Gly	Gln	Glu				
305					310				315					320					
Glu	Ser	Leu	Asp	Ser	Phe	Thr	Ser	Asn	Asn	Gly	Pro	Phe	Gln	Tyr	Tyr				
			325					330						335					
Leu	Gly	Gly	His	Ser	Ser	Gln	Pro	Met	Glu	Asn	Ser	Gly	Phe	Arg	Glu				
		340						345					350						
Asp	Ile	Gln	Val	Pro	Pro	Gly	Asn	Gly	Asn	Ile	Gly	Asn	Met	Gln	Val				
	355					360						365							
Val	Ala	Val	Glu	Gly	Lys	Gly	Glu	Val	Lys	His	Gly	Gly	Glu	Asp	Gly				
	370					375					380								
Arg	Asn	Asn	Ser	Gly	Ala	Pro	His	Arg	Glu	Lys	Arg	Gly	Gly	Glu	Thr				
385					390				395					400					
Asp	Glu	Phe	Ser	Asn	Val	Arg	Arg	Gly	Arg	Gly	His	Arg	Met	Gln	His				
			405					410					415						
Leu	Ser	Glu	Gly	Thr	Lys	Gly	Arg	Gln	Val	Gly	Ser	Gly	Gly	Asp	Gly				
		420						425					430						
Glu	Arg	Trp	Gly	Ser	Asp	Arg	Gly	Ser	Arg	Gly	Ser	Leu	Asn	Glu	Gln				
	435					440					445								
Ile	Ala	Leu	Val	Leu	Met	Arg	Leu	Gln	Glu	Asp	Met	Gln	Asn	Val	Leu				
	450					455					460								
Gln	Arg	Leu	Gln	Lys	Leu	Glu	Thr	Leu	Thr	Ala	Leu	Gln	Ala	Lys	Ser				

465                      470                      475                      480  
 Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln Arg Pro  
                                  485                      490                      495  
 Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu Thr Phe Ala Ile  
                                  500                      505                      510  
 Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr Leu Tyr Tyr Gln Arg  
                                  515                      520                      525  
 Arg Arg Arg Lys Leu Asn  
                                  530

<210> 25  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:chemically  
                                  synthesized

<400> 25  
 agatctgacg aggatgagaa cagcccg                      27

<210> 26  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:chemically  
                                  synthesized

<400> 26  
 ctcgtcgtcg acgcaggcag ctatctccgc ctggtttttg tg                      42

<210> 27  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:chemically  
                                  synthesized

<400> 27  
 ctcgtcctcg agggtaagcc tatccctaac                      30

<210> 28  
 <211> 31  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chemically synthesized

<400> 28

ctcgtcgggc ccctgatcag cgggtttaa c

31

<210> 29

<211> 36

<212> DNA

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<220>

<223> Description of Artificial Sequence:chemically synthesized

<400> 29

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36

<210> 30

<211> 33

<212> DNA

<213> Artificial Sequence

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<400> 30

ctcgagacag ccgctccgtc ggccaggcca tgt

33

<210> 31

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<220>

<223> Description of Artificial Sequence:chemically synthesized

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39

<210> 32

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<223> Description of Artificial Sequence:chemically synthesized

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synthesized

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<210> 34  
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synthesized

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<210> 36  
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<210> 37  
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<400> 37  
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<210> 38  
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synthesized

<400> 38  
caggcacact gaccattcga 20

<210> 39  
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<400> 39  
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<210> 40  
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synthesized

<400> 40  
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<210> 41  
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<400> 41

cagaggaagg atccagtgtg tgt

23

<210> 42

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:chemically synthesized

<400> 42

catggagtat ggatctggaa atagtc

26

<210> 43

<211> 25

<212> DNA

<213> Artificial Sequence

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cagagcgccc tccctgtacc acaaa

25

<210> 44

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<212> DNA

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20

<210> 45

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20

<210> 46

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<212> DNA

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<400> 46

ttcaggcatc tgcaacctcc gtgg

24

<210> 47

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<212> DNA

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<400> 47

aggacatagg atgcaacact tgag

24

<210> 48

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<212> DNA

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ccagcgctcc ccatcac

17

<210> 49

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:chemically  
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<400> 49

acctgccggc ccttggttcc t

21

*Q1  
Concise*